Mon Aug 12 17:16:21 2002

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GenCore version 4.5
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OM protein - protein search, using sw model

August 12, 2002, 17:19:43 ; Search time 27.08 Seconds (without alignments) 28.387 Million cell updates/sec Run on:

10-071247-1 59 Perfect score: Title:

1 думдкдум 8 Scoring table: Sedneuce:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_71:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	killer toxin resis	short-chain fatty	hypothetical prote			_		_	hypothetical prote	acetyltransferase	conserved hypothet	probable formylmet	mannosyl-glycoprot	beta-N-acetylhexos	beta-N-acetylhexos	Ig heavy chain V r	transposase - Dein	hypothetical prote	DNA ligase (ATP) (hypothetical prote		saposin precursor	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	hypothetical prote	hypothetical prote
	ID	BVBYK5	F83694	E69903	G83047	H83554	B72567	AC2394	D83812	A83915	AE2918	H97692	A69491	A56390	E95006	A97879	PH1663	F75337	AI2041	137079	863669	S77357	AD1927	A28716	B29514	A29476	S01114	S47572	S73827	B72742
	BB :	Н	7	7	7	7	~	7	7	7	7	7	~	7	~	~	7	~	~	7	7	7	7	П	7	7	7	~	~	7
	Length	1365	441	83	187	358	470	80	180	181	196	207	563	1311	1312	1312	113	145	375	844	1447	489	495	554	589	589	590	590	741	102
* Query	Match	7.67	76.3	73.7	73.7	72.9		71.2		71.2			71.2		71.2	71.2	69.5	69.5	69.5	69.5	69.5	67.8	67.8	67.8	67.8	67.8	8. 79	67.8	67.8	66.1
	Score	47	45	B	43.5	43	43	42	42	42	42	42	42	42 ^	42	42	41	41	41	43	41	40	40	40	40	40	40	40	40	39
Result	NO.	1	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A.Gene: SGD:KRE5; MIPS:YOR336w
A.Cross-references: SGD:S0005863; MIPS:YOR336w
A.Map position: 15R
A.Map position: 15R
C.Function: A.Description: required for normal cell growth
A.Pathway: (1->6)-beta-D-glucan biosynthesis
C.Superfamily: KRE5 protein
C.Superfamily: KRE5 protein
F.1-17/Domain: signal sequence #status predicted <SIG>F:1-17/Domain: signal sequence #status predicted <SIG>F:18-1365/Product: killer toxin resistance protein KRE5 #status predicted <MAT>

acetyltransferase,	conserved nypotnet acetyltransferase,	hypothetical prote	hypothetical prote	secretory protein-	probable heme tran	probable phosphoes	hypothetical prote	hypothetical prote	INDAl protein - fu	cyclomaltodextrin	probable membrane	G protein-coupled	probable ABC trans	protein F18014.29
D87288	B97933 A95066	H22845	826009	T47883	S70854	G83242	T04561	T36462	S33212	ALKBG	S67568	JC5808	E95268	B86328
20	7 (7	7	7	7	Н	Н	7	7	Н	-	a	~	7	7
177	186	194	228	247	250	270	396	499	573	655	961	962	273	115
66.1	00.T	66.1	66.1	66.1	66.1	1.99	66.1	66.1	66.1	66.1	66.1	66.1	65.3	64.4
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30	32 32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 BVBXK5
	killer toxin resistance protein KRE5 precursor – yeast (Saccharomyces cerevisiae) N;Alternate names: protein 06254; protein YOR336w
	C;Species: Saccharomyces cerevisiae C:Date: 30-Sep-1991 #sequence revision 10-May-1996 #text change 16-Jun-2000
_	C, Accession: \$62066; A36327; S67243; S71974; \$12202
_	Rivatie, A.G.; Hand, N.J.; Goulding, S.G.; Wolle, K.H. submitted to the KMR. Data Library. June 1967
	A; Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sa
	A; Reterence number: S62058 A: Accession: S62066
	A; Molecule type: DNA
	A;Residues; 1-136 SPAR. A:rccs-references: FMR:.746821 MTD.01163062 DTDN.CAA89981 1: DTD.01164070
	R. Medden, P., Hill, K.; Magner, J.; Slipetz, D.; Sommer, S.S.; Bussey, H.
_	Mol. Cell. Biol. 10, 3013-3019, 1990
	A; Title: The yeast KRE5 gene encodes a probable endoplasmic reticulum protein require
_	A:Keterence unuber: A303Z/; MULD:9UZ5889Z A:Acression: A36327
	A WOLCOLD TO THE TOP T
_	A; Residues: 1-581,581,583-779,11,781,1KMKCOKONISK',794,'K',795-1365 <mea></mea>
_	A; Cross-references: EMBL: M33556; NID: 9171794; PIDN: AAA34725.1; PID: 9171795
	R;Goulding, S.E.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.
	submitted to the Protein Sequence Database, July 1996
	A) Accession: 567243
_	A; Molecule type: DNA
	A; Residues: 1-1365 < GOU>
	A; Cross-references: EMBL: Z75244; NID: 91420730; PIDN: CAA99659.1; PID: 91420731; GSPDB:G
	A:Experimental source: strain S288C
	K;Farie-Modermott, A.G.; Hand, N.J.; Goulding, S.E.; Wolfe, K.H. Yeast 12. 999-1004. 1996
_	Ailitle: Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces c
	A; Reference number: S71966; MUID:97051586
_	A; Accession: S71974
	A;Status: nucleic acid sequence not shown; translation not shown
	A; Molecule type: DNA
	A; Residues: 1-1365 <- PAW>
	A)CIOSS TEIETENECES: EMBL:24981; NID:GILG5002; PIDN:GAR9981.1; PID:GILD500.0 A.NOTE: the nucleocestide commence use submitted to the mark nata 1; heart 1006.
	A, Note: the introduction equation was submitted to the Embi variables; ours 1990 C;Genetics:

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Gaps

ä

Indels Length

; 0

Mismatches

DB 2;

Score 43.5; DI Pred. No. 8.5;

Hickey, Larbig,

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683047
hypothetical protein PA4793 [imported] - Pseudomonas aeruginosa (strain PAO1)
c;Species: Pseudomonas aeruginosa
c;Species: Pseudomonas aeruginosa
c;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
c;Accession: 683047
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbis, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                73.7%;
87.5%;
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                                                                                                                                                 Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-187 <STO>
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                                                                        Query Match
Best Local Similarity
Matches 7; Conser
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E6903
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, B.; Capuano, V.; Carter, N.M.; Chc
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fumaro, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Evine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.H.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Scklguchi, J.; Sckowska, A.; Scorlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Scklguchi, J.; Sckowska, A.; Serol
A;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Anceleicher Phocons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspertance of the sequence of the albability bacillus halodurans (strain C-125) c; Species: Bacillus halodurans c; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 c; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 c; Accession: F83694 c; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132 c; Ascession: F83594 Ascession: F8359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:299114; GB:AL009126; NID:92634230; PIDN:CAB13852.1; PID:e1185432;
A,Experimental source: strain 168
                                          9
F:1362-1365/Region: endoplasmic reticulum retention signal #status predicted F:115,228,293,457,519,523,604,644,870,1091,1150,1195/Binding site: carbohydrate (Asn)
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1.93 <KGN>
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C;Superfamily: conserved hypothetical integral membrane protein HP0693
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Pred. No. 31;
1; Mismatches
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Pred. No. 22;
2; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                              Query Match 79.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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48 YWGEGFW 54
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A;Gene: yodI
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F83694
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hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: #83554
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
R; Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID:20437337
A; Accession: #8354
A; Accession: #8354
A; Accession: #8354
A; Residues: preliminary
A; Rollecule type: DNA
A; Residues: 1-358 < ATO>
A; Residues: 1-358 < ATO>
A; Residues: 1-358 < ATO>
A; Residues: 1-358
A; Residues: 1-358
A; Residues: Lasin PA01
C; Genetics:
A; Gene: PA0736
                                                                                                                                                       A;Cross-references: GB:AE004892; GB:AE004091; NID:g9951049; PIDN:AAG08179.1; GSPDB:GN A;Experimental source: strain PAO1
C;Genetics:
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337 A;Accession: G83047
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                                                                                                                                                                                                                                                                                                                                                       73.7%; Score 43.5; L
87.5%; Pred. No. 17;
ive 0; Mismatches
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-180 <STO>
A, Residues: 1-180 <STO>
A, Cross references: GB. AP001511; GB: BA000004; NID:g10173727; PIDN: BAB05019.1; GSPDB:G
A, Experimental source: strain C-125
C, Genetics:
A, Genetics:
A, Genetics:
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                                                                                                                                                                                                                                                                 71.2%; Score 42; DB 100.0%; Pred. No. 28; ive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                    Query Match 71.2
Best Local Similarity 100.
Matches 6; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-196 <KUR>
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                                                              hypothetical protein APE1820 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Description 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72567
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takarainya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Accession: B72567
A;Status: preliminary
A;Accession: B72567
A;Status: preliminary
A;Accession: B72567
A;Status: DabJ:AP000062; NID:95105244; PIDN:BAA80823.1; PID:95105510
A;Ecsiques: 1-470 < KAWA
A;Resiques: 1-470 < KAWA
A;Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80823.1; PID:95105510
C;Genetics:
A;Gene: APE1820
C;Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; messento, messento, messento, messento, s.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B. 205-213, 2001

NA Res. 8, 205-213, 2001

A; Aitile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A; Reference number: AB1807; MUID:2159285; PMID:11759840

A; Accession: AC2394

A; Accession: AC2394

A; Molecule type: DNA

A; Residues: 1-80 < KUR>
A; Molecule type: DNA

A; Residues: 1-80 < KUR>
A; Cross references: GB:BA000019; PIDN:BAB76406.1; PID:g17133844; GSPDB:GN00179

A; Cross references: strain PCC 7120
C; Genetics:
A; Gene: asr4707
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Date 1000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: DB3812
R;Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Feference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein asr4707 [imported] - Anabaena sp. (strain PCC 7120)
C; Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: Ac2394
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Ir
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46;
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Pred. No. 46;
1; Mismatches
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Pred. No. 13;
0; Mismatches
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85.7%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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329 WGRGYW 334
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D83812
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RESULT 9
A83915
hypothetical protein BH2121 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83915
R;Takami, H: Nakasone, K; Takaki, Y: Maeno, G:; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Accession: A83915
A;Genetics: 1-181 <STOO
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05840.1; GSPDB:C,Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 11-3an-2002
C;Accession: AE5918
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC1
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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A;Experimental source: strain C58 (Dupont)
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. 28;
       Length 180;
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                                                                       0; Indels
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DB
28;
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Gaps

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C; Species: Streptococcus pneumoniae
C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C; Accession: A56390
A; Title: Cloning and expression of the beta-N-acetylglucosaminidase gene from Strepto A; Reference number: A56390; MUID:95238375
A; Accession: A56390
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1311 <CLA>
A; Residues: 1-1311 <CLA>
A; Coss.references: GB:L36923; NID:g784896; PIDN:AAC41450.1; PID:g784897
C; Generics:
A; Gene: strH
C; Keywords: glycosidase; hydrolase; tandem repeat
F; 1-33/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Accession: E95006
R; Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
nson, T.; Hickey, E.K.; Hollt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Residues: L1312 < KURP>
A; Residues: 1-1312 < KUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005672; PIDN:AAK74246.1; PID:914971522; GSPDB:GN00164; TIGR:A;Experimental source: strain TIGR4 C;Genetics: A;Genetics: A;Genes: SP0057
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97872
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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71.48;
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Best Local Similarity 71.4
Matches 5; Conservative
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Richershin: no.3.3.1

Richershin: no.3.3.1

Richershin: no.3.3.1

Richershin: no.3.3.1

Richershin: R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364.370, 1997

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A; Reference number: A69250; MUID: 98049343

A; Recession: A69491

A; Residues: 1-563 «KLE»

A; Residues: 1-563 «KLE»

A; Residues: 1-563 «KLE»

A; Reciderences: GB: AEC00070; GB: AEC000782; NID: 92689293; PIDN: AAB89325.1; PID: 9264861

C; Superfamily: formylmethanofuran dehydrogenase (molybdenum) alpha chain

C; Keywords: iron-sulfur protein; molybdenum; molybdepterin; oxidoreductase; tungsten
                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: H97692
A; Liu, F; Wollam, C; Allinger, M.; Doughty, D.; Scott, C; Lappas, C; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
A; Accession: H97692
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-207 < KUR>
A; Residues: 1-207 < KUR>
A; Cross-references: GB: AE007869; PIDN: AAK88497.1; PID:g15158008; GSPDB: GN00169
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A56390
mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - Strept
                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein BH0837 (AP001510) [imported] - Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum/tungsten) chain A C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: A69491
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A;Map position: circular chromosome
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A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-1312 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK98861.1; PID:g15457590; GSPDB:GN00174
C;Genetics:
A;Gene: strH
C;Keywords: glycosidase; hydrolase
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Gaps 0; Query Match 71.2%; Score 42; DB 2; Length 1312; Best Local Similarity 71.4%; Pred. No. 1.6e+02; Matches 5; Conservative 1; Mismatches 1; Indels 2 ywgkgyw 8 || ||:| 871 YWSKGWW 877 οp δy

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Search completed: August 12, 2002, 17:22:44 Job time: 181 sec

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Page 1

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August 12, 2002, 17:21:48; Search time 13.51 Seconds (without alignments) 22.928 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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59
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sacchar		Q9f5n7 burkholderi			O13035 gallus gall		Q9erz3 mus musculu	P08483 rattus norv	P41984 bos taurus	3	P75443 mycoplasma	_	•	_	Q9j5c7 fowlpox vir		P50482 oryctolagus	Q9uby0 homo sapien	P48763 rattus norv	Q62556 mus musculu	P18892 bos taurus		Q57223 haemophilus	_	_	P44051 haemophilus			Q12899 homo sapien	P54148 synechocyst	09332 dros	P33622 mus musculu
SUMMARIES	DI	[2]	STRH_STRPN	NORM_BURVI	DNL4_HUMAN	UGGG_SCHPO	SAP_CHICK	SAP_RAT	ACM3_MOUSE	ACM3_RAT	ACM3_BOVIN	ACM3_PIG	YD35_MYCPN	YM05_MARPO	INA1_TRIHA	CDGT_KLEPN	V093_FOWPV	PLD_CORPS	NAH2_RABIT	NAH2_HUMAN	NAH2_RAT	BUTY_MOUSE	BUTY_BOVIN	BUTY_HUMAN	YD14_HAEIN	PLYD_ERWCA	HEMN_MYCTU	ATOE_HAEIN	PSBB_SYNY3	PSBB_SYNP7	Z173_HUMAN	Y537_SYNY3	UGGG_DROME	APC3_MOUSE
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Q45537 bacillus su P17989 fibrobacter P80011 rhizobium m P55620 rhizobium s Q44678 corynebacte P76460 escherichia P50430 rattus norv O78511 guillardia P15848 homo sapien Q9n2a3 gorilla gor P20309 homo sapien Q9n2a4 pan troglod		THE SELUT: ID RESELVENT ID REPERSONANCE STANDARD; PRT; 1365 AA. PRT (RESELVENT PROBLES PEAST PROBLES PEAST O1-NOW-1997 (Rel. 15; Lest sequence update) O2-NOW-1997 (Rel. 15; Lest sequence update) O3-NOW-1997 (Rel. 15; Lest sequence update) O4-NOW-1997 (Rel. 15; Lest sequence update) O5-NOW-1997 (Rel. 16; Lest sequence update
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holl I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATC (12213)
STRAIN=ATC (12213)
MEDINE-95238375; PubMed=7721787;
Clarke V.A., Platt N., Butters T.D.;
"Cloning and expression of the beta-N-acetylglucosaminidase gene from Streptococcus pneumoniae. Generation of truncated enzymes with modified aglycon specificity.";
                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
PREVENT SECRETION FROM BR.
MISSING (NREF. 1).
HLDONEVPETEHFEA -> ILIKMKCQKQNISKAK (IN
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
-!- SIMILARITY: BELONGS TO FAMILY 20 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                        (POTENTIAL).
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0
             (POTENTIAL)
                                                                                                                                                           Score 47; DB 1; Length 1365; Pred. No. 7.1; 1; Mismatches 1; Indels
                                                                                                                         DOF5851175CC0333 CRC64;
                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-N-acetylhexosaminidase precursor (EC 3.2.1.52).
                    N-LINKED (GLCNAC. ..)
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 (GLCNAC. .
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 N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
                                                                                                                          1365 AA; 156476 MW;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                CATALYTIC DOMAIN 2. CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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"Cloning and characterization of norM, encoding a multi-drug efflux protein from Burkholderia vietnamiensis.";
Submitted (OCT-2000) to the EMBL/Genbank/DDBJ databases.
-i- FUNCTION: FUNCTIONS AS. A NA(+)/DRUG ANTIPORTER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
-i- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE) FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable multidrug resistance protein norM (Na(+)/drug antiporter)
                                                       InterPro; IPR001540; Glyco_hydro_20.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00728; Glyco_hydro_20; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Hydrolase; Glycosidase; Repeat; Transmembrane; Cell wall; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
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Pred. No. 39;
                                                                                                                                                                                                                                                BETA-N-ACETYLHEXOSAMINIDASE.
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CATALYTIC DOMAIN 1.
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7 -> E (IN REF. 1).
7 -> A (IN REF. 1).
7 -> A (IN REF. 1).
8 -> K (IN REF. 1).
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16-007-2001 (Rel. 40, Last sequ
16-007-2001 (Rel. 40, Last anno
              AE007323; AAK74246.1; -. SP0057; -.
EMBL; L36923; AAC41450.1; -.
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Best Local Similarity 71.4%;
Matches 5; Conservative
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UGGG_SCHPO
Q09140;
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BINDING
SEQUENCE
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UGGG_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Prostate;
MEDLINE-92580920; PubMed-7760816;
MEDLINE-95280920; PubMed-7760816;
Wei Y.-F., Robins P., Carter K., Caldecott K., Pappin D.J.C.,
Yu G.-L., Wang R.-P., Shell B.K., Nash R.A., Schar P., Barnes D.E.,
Haseltine W.A., Linddahl T.;
"Molecular cloning and expression of human cDNAs encoding a novel DNA
ligase IV and DNA ligase III, an enzyme active in DNA repair and
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel, 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase IV (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
ISSUE SPECIFICITY: TESTIS, THYMUS, PROSTATE AND HEART.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
SIMILARITY: COUNTAINS 2 BRCT DOWAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                             Transport; Sodium transport; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                               Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + {decxyribonuclectide}(N) + {decxyribonuclectide}(M) = AMP + diphosphate + {decxyribonuclectide}(N+M).
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844 AA.
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Pred. No. 21;
0; Mismatches
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send an email to license@isb-sib.ch).
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InterPro; IPR000977; DNA_ligase.
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01-OCT-1996 (Rel. 34, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                        MM;
                                  EMBL; AF312031; AAG27731.1; -
InterPro; IPR002528; UPF0013.
Pfam; PF01554; UPF0013; 2.
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58.3%;
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Best Local Similarity 58.3.
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192
222
267
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345
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                                                                                                                                                                                                                                                                                                                      462 AA;
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1147
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Mol. Cell. Bio
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P49917;
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Pfam, PF00533; BRCT; 2.

Pfam, PF01068; DNA_ligase; 1.

SMART; SM00292; BRCT; 2.

PROSITE; PS00697; DNA_LIGASE_A1; 1.

PROSITE; PS00697; DNA_LIGASE_A2; 1.

PROSITE; PS001333; DNA_LIGASE_A3; 1.

PROSITE; PS00133; DNA_LIGASE_A3; 1.

DNA repair; DNA replication; DNA recombination; Cell division; Ligase; ATP-binding; Nuclear protein; Repeat.

DOMAIN 587 676 BRCT 1.

TAL 844 BRCT 1.
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J. Biol. Chem. 269;30701-30706(1994).
-1- FUNCTION: UNFOLDED, DENATURED GLY.
BETTER SUBSTRATES FOR GLOCOSYLATION BY THIS ENZYME THAN ARE THE CORRESPONDING NATIVE PROFEINS. THIS PROTEIN AND TRANSIENT GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING THE FOLDING AND ASSEMBLY OF NUMEY. MADE GLYCOPROTEINS, IN ORDER TO IDENTIFY GLYCOPROTEINS THAT NEED ASSISTANCE IN POLDING FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fernandez F., Jannatipour M., Hellman U., Rokeach L.A., Parodi A.J.; "A new stress protein: synthesis of Schizosaccharomyces pombe UDP--GL:Glycoprotein glucosyltransferase mRNA is induced by stress conditions but the enzyme is not essential for cell viability."; EMBO J. 15:705-713(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
UDP-glucose:glycoprotein glucosyltransferase precursor (EC 2.4.1.-)
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Fernandez F.S., Trombetta S.E., Hellman U., Parodl A.J.;
"Purification to homogeneity of UDP-91ucose:glycoprotein
glucosyltransferase from Schizosaccharomyces pombe and apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: REQUIRES CALCIUM AND MANGANESE IONS FOR ACTIVITY.
-!- PATHWAY: GLYCOSYLATION.
-!- SUBUNIT: MONOMER.
-!- SUBCELLUTAR LOCATION: Endoplasmic reticulum lumen.
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MEDLINE-96181349; PubMed-8631292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%; Score 41; DB 1; Length 844; 100.0%; Pred. No. 37; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood V., Warren T., Harris D., Barrell B.G., Rajandream Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                AMP (BY SIMILARITY).
D4BE16F211A3BE97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Edwaryota: Fungi, Ascomycota: Schizosaccharomycetels; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UDP-Glc:glycoprotein glucosyltransferase). GPT1 OR SPBPJ4664.06.
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SEQUENCE FROM N.A.
STRAIN=972;
Wood V., Warren T.,
                                                                                                                                                                                                                                                                                                                                                                                                               844 AA;
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Best Local Similarity
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16-OCT-2001 (
01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altman N., Horowitz M.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proactivator polypeptide precursor [Contains: Saposin A; Saposin B; Saposin C; Saposin D].
                                                                                                                                                                                                                                                            N-LINED (GLCNAC...) (POTENTIAL).
T-N-LINED (GLCNAC...) (POTENTIAL).
                                                                                                                                                  EMBL, AL591302; CAC38351.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Signal; Transferase; Glycosyltransferase; Endoplasmic reticulum;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 AA.
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1; Mismatches
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                                                                                                                                          EMBL; U38417; AAB05993.1; -.
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    -! - PTM: GLYCOSYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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Best Local Similarity
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NCBI_TaxID=9031;
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                                                                                                                                                                                                            Glycoprotein.
SIGNAL
CHAIN 1
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013035;
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SAP_CHICK
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THE SHILMOLIPIES ACTIVATION PROPERTIES (COPPOSITION); HE SHILMARTY).

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                         Gaps
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MEDLINE=56175345; PubMed=8601692;
MEDLINE=56175345; PubMed=8601692;
MEDLINE=56175345; PubMed=8601692;
MEXPIESSAOn and tissue distribution of rat sulfated glycoprotein-1 (prosaposin).";
J. Histochem. Cytochem. 44:327-337(1996).
-i. SUBCELLUAR LYCOATION: Extracellular.
-i. SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
-i. SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96128541; Pubmed-8573994;
Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
"Molecular role of sulfated glycoprotein-1 (SGP-1/prosaposin) in
Sertoli cells.";
Histol. Histopathol. 10:1023-1034(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Sertoli cells;
MEDLINE-89000647; PubMed-3048385;
Collard M.W., Sylvester S.R., Tsuruta J.K., Griswold M.D.;
"Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat Sertoli cells: sequence similarity with the 70-kilodalton precursor to sulfatide/GMI activator.";
Biochemistry 27:4557-4564(1988).
                                                                                                                         ;
                                                    Score 40; DB 1; Length 518;
Pred. No. 33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  SAP_RAT STANDARD; PRT; 554 AA. 101960; 062841; 064190; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 801fated 91ycoprotein 1 precursor (SGP-1) (Prosaposin). PSAP OR SGPI.
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InterPro: IPR003119; SapA.
InterPro: IPR000004; SapB.
InterPro: IPR003259; Saposin.
Pfam; PF02199; SAPA; 2.
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ProDom; PD012321; Saposin; 1.
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                                                       67.8%;
83.3%;
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                                                    Query Match 67.8
Best Local Similarity 83.3
Matches 5; Conservative
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SMART; SM00118; SAPB; 4.
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TISSUE-Brain;

MEDLINE=5517920; PubMed=7874308;

Andre C., Dos Santos G., Koulakoff A.;

"Cultured neurons from mouse brain reproduce the muscarinic receptor profile of their tissue of origin.";

Eur. J. Neurosci. 6:1691-710(11994).

-I- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADDRIVATE CYCLASE, BREAKDOWN OF PHOSPHOINOSTIDES, MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 3.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 5.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                           SULFATED GLYCOPROTEIN 1.
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09ERZ3; 064055;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Muscarinic accyylcholine receptor M3 (Mm3 mAChR).
CHRM3 OR CHRM-3.
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Pred. No. 3
    Glycoprotein; Repeat.
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83.3%;
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Best Local Similarity 83.30,
best 5; Conservative
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                                         Mus musculus (Mouse).
                             SEQUENCE FROM N.A.
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                    SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
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N-LINKED (GICNAC. .) (POTENTIAL).

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N-LINKED (GICNAC. .) (POTENTIAL).

N-LINKED (GICNAC. .) (POTENTIAL).
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Pred. No. 38;
0; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                            SUBCELLULAR LOCATION: Integral membrane protein.
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01-AUG-1988 (Rel. 08, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CHRM3 OR CHRM-3.
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Best Local Similarity 71.4
Matches 5; Conservative
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Wess J., Maggio R., Palmer J.R., Vogel Z.;
Wess J., Maggio R., Palmer J.R., Vogel Z.;
Wess J., Maggio R., Palmer J.R., Vogel Z.;

"Role of conserved threonine and tyrosine residues in acetylcholine
binding and muscarinic receptor activation. A study with m3
muscarinic receptor point mutantes.";
J. Biol. Chem. 267:19313-19319(1992)
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
-: CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Braun T., Schofield P.R., Shivers B.D., Pritchett D.B., Seeburg P.H.; "A novel subtype of muscarinic receptor identified by homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Furuta M., Ohya S., Imaizumi Y., Watanabe M.;
"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wess J., Gdula D., Brann M.R.;
"Site-directed mutagenesis of the m3 muscarinic receptor:
identification of a series of threonine and tyrosine residues
involved in agonist but not antagonist binding.";
EMBO J. 10:3729-3734(1991).
                                                                                                                                                   Bonner T.I., Young A.C., Brann M.R., Buckley N.J.; "Cloning and expression of the human and rat m5 muscarinic
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modified and this statement is not removed entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
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PRINTS; PR00237; GPCRHDODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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GCRDb; GCR_0118; -.
GCRDb; GCR_0119; -.
GCRDb; GCR_0140; -.
Interpro; IPR000276; GPCR_Rhodpsn.
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EMBL; MI6408; AAA40662.1; ALT_SEQ.
EMBL; MI8088; AAA40659.1; ...
EMBL; MG2826; AAA41553.1; ...
EMBL; AB017656; BAA36839.1; ...
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                                                                                                                     MEDLINE=90166521; PubMed=3272174;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88077068; Pubmed=3120722;
                                                                                                                                                                                                                                   acetylcholine receptor genes.";
Neuron 1:403-410(1988).
Science 237:527-532(1987).
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PIR; A29476; A29476.
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Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE WUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
                                                                                                                                                                             7 (POTENTIAL).
CYDOPLASNIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
A -> R (IN REF. 4).
C -> R (IN REF. 4).
T -> M (IN REF. 3).
T -> M (IN REF. 3).
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              receptor.
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MEDILINE-94339178; PubMed-8061048;
MEDINE-94339478; P.K., Glickman F., Chang K.J.;
Lee P.H., Hodges P.K., Glickman F., Chang K.J.;
"Cloning and expression of a cDNA encoding bovine muscarinic
                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 589;
Pred. No. 38;
                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
          Phosphorylation; Multigene family; G-protein coupled recomment 1 66 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last annotation update)
Muscarinic acetylcholine receptor M3.
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Biochim. Biophys. Acta 1223:151-154(1994).
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01-NOV-1995 (Rel. 32, Last seq
15-JUL-1998 (Rel. 36, Last anno
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71.4%;
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                        Best_Local Similarity
Matches 5; Conserv
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P41984;
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EXPRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

A - S (IN REF. 2).

A -> G (IN REF. 2).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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EXTRACELLUIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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38;
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3.
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71.4%;
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461
467
590 AA;
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                                                                FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING IMPLIBITION OF ADENTARE CYCLASE, BREAKOWN OF PHOSPHOTNOSITIDES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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   MEDIINE-88296835; PubMed-3402600;
Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.;
"Primary structure of porcine muscarinic acetylcholine receptor III
and antagonist binding studies.";
FEBS Lett. 235.257-261(1988).
                                                                                                                                                                                                                                                      EMBL; X14/14; S01114; S01114.

GCRDb; GCR_0104; -

InterPro; IPR000276; GPCR_Rhodpsn.

PRIM: PRO001; 7tm_1; 1.

PROSITE; PRO0237; GPCRRHODPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00263; G_PROTEIN_RECEP_F1_2; 1.

PROSIPATION: Multigene family; G-Protein coupled receptor.

EXTRACELLULAR (POTENTIAL).
                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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(Rel. 35, Last sequence update)
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CYTOPLASMIC (F
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N-LINKED
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Marchantiales; Marchantiaceae; Marchantia.
                                                                                                                                                                                                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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J. Mol. Biol. 223:1-7(1992).
                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.PNEUMONIAE MPN333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                             Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                               Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 741;
46;
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 26.5 kDa protein in RPS2 3'region (ORF 228).
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1776A96BCF83567F CRC64;
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical protein MPN335 (F10_orf741).
MPN335 OR MP501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB96149.1;
LUCETPIO; IPR00188; GABAA.Feceptor.
Pfam; PF02932; Neur_chan_memb; 1.
Hypothetical protein; Transmembrane.
TRANSMEM
76
TANSMEM
77
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Pred. No.
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; Pubmed=8948633;
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nilarity 71.4%;
Conservative 0
                                                                                                                               Mycoplasmataceae; Mycoplasma
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176
207
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Best Local Similarity
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715
741 AA;
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                                                                                                                                                       NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-IMI 206040;
MEDLINE-95291429; PubMed-7773384;
Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma harzianum genes induced during growth on Rhizoctonia
                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBL_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solani cell walls.";
Microbiology 141:767-774 (1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: DURING MYCOPARASITISM.
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 228;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                     EMBL; M68929; AAC09463.1; -.
PIR; $26009; $26009.
Mendel; 2116; Marpo; ymf5;1.
InterPro; IPR002541; CytC_asm.
InterPro; IPR003557; CytC_biog_CcmC.
Pfam; PF01578; CytC_asm; 1.
PRINTS; PR01386; CCMCBIOGNSIS.
Mitochondrion; Hypothetical protein.
SEQUENCE 228 AA; 26461 MW; BF13C3616D6C7D35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Amino-acid transport; Transmembrane.
TRANSMEM 72 92 POTENTIAL.
TRANSMEM 99 117 POTENTIAL.
TRANSMEM 176 200 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-07-1996 (Rel. 34, Last annotation update)
Amino-acid permease INDA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 AA
                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S33212; S33212.
InterPro; IPR002293; AA_rel_permease_1.
TnterPro; IPR002027; Amino_acid_permease.
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62.58;
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 62.5
nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binder F., Huber O., Boeck A.;
"Cyclodextrin-glycosyltransferase from Klebsiella pneumoniae M5al:
"Cyclodextrin-glycosyltransferase from Klebsiella pneumoniae M5al:
"Cloning, nucleotide sequence and expression.";
Gene 47:269-277(1986).
-i. CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
(Cyclodextrin-glycosyltransferase) (CGTase).
                                                                                                                                                                                                                                                Score 39; DB 1; Length 573;
                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                POTENTIAL.
5FB0A806934DB55D CRC64;
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Transferase; Glycosyltransferase; Calcium; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                   POTENTIAL.
  POTENTIAL
                         POTENTIAL.
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HSSP, P30920. 1GCT.
INTERPRO; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
Pfam; PF00128 alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
Pfam; PF00686; CBD_4; 1.
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MEDLINE=87163498; PubMed=2951300;
                                                                                                                                                                        62850 MW;
                                                                                                                                                                                                                                                66.1%;
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280
315
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527
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257
296
351
398
425
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573 AA;
                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         239 YWGARYW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=573;
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P08704;
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                    TRANSMEM
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CDGT_KLEPN
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Matches
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GLUCANOTRANSFE			
31 655 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE 253 253 BY SIMILARITY. 287 287 BY SIMILARITY. 363 363 BY SIMILARITY. 655 AA, 73024 MW; DB8F26332BED26A7 CRC64;	Query Match 66.1%; Score 39; DB 1; Length 655; Best Local Similarity 62.5%; Pred. No. 59; Matches 5; Conservative 2; Mismatches 1; Indels		Search completed: August 12, 2002, 17:27:25
655 253 287 363 73024 M	66.1%; 62.5%; rative		12, 200
31 253 287 363 655 AA;	milarity Conserv	9yw 8 : DYF 129	d: August
CHAIN ACT_SITE ACT_SITE ACT_SITE SEQUENCE	ery Match st Local Si tches 5;	1 gywgkgyw 8 : : 22 GYWGRDYF 129	Search completed:
FT FT FT SQ	Qu Be Ma	Qy	Sear

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Q9emt5 amsacta moo Q9rt39 deinococcus Q90yb1 gallus gall P95462 plectonema Q9ftg0 oryza sativ P73420 synechocyst Q9fw6 aeropyrum p Q01150 magnaporthe Q9n15 magnaporthe Q9n19 pasteurella Q9sb4 caulobacter Q97s47 streptococc Q91zz1 arabidopsis Q97z47 arabidopsis Q952d9 streptomyce Q91053 streptomyce Q91053 streptomyce Q91053 streptomyce Q91053 streptomyce Q91053 streptomyce Q91051 streptomyce Q920103 streptomyce Q91051 streptomyce Q920103 streptomyce

0930z1 rhizobium m 00833 mertones un 091n41 arabidopsis 093wke arabidopsis 095z8 cynomys lud 095zx8 sulfolobus

O9wuj4 mus musculu

protein

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Run ĕ

Sequence:

Searched:

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PERAIN-DSM 1728;

MEDLINE-20479972; PubMed=11029001;

Ruppp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;

"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";

Nature 407:508-513(2000).

BENBL: AL445063; CAC11406.1; -.

Hypothetical protein; Complete protecome.

SEQUENCE 748 AA; 82250 MW; 73A030A0E217EE39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 17; Length 748;
Pred. No. 25;
0; Mismatches 1; Indels
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Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                   P95462
Q9FTG0
P73420
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Q9CN19
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Q962X8
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Q9HZ21
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O08939
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Q12361
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Similarity 85.7%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
NCBI_TaxID=2303;
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| 532 YWGKAYW 538
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Q9HLG7
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RESULT
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Q9KFW3
ID Q9
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Q9axa8 oryza sativ
Q9h1f3 thermoplasm
Q3h5f4 bacilius su
Q9h15 pseudomonas
Q9f3t0 rhodothermu
Q9i5j3 pseudomonas
Q9yax5 aeropyrum p
Q9vnf1 drosophila
Q21906 bacteriopha
Q9kdb3 bacillus ha
Q9kdb1 bacillus ha
Q9kdb1 bacillus ha
Q9kdb1 bacillus ha
Q9kdb1 bacillus ha
Q9kdb3 aciallus ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9hlg7 thermoplasm
Q9kfw3 bacillus ha
Q9h5j0 homo sapien
                                                                  (without alignments)
33.236 Million cell updates/sec
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                                                        August 12, 2002, 17:22:13 ; Search time 41.64 Seconds
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                                                                                                                                                                            562222
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                       562222 seqs, 172994929 residues
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                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
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Q34654
Q9HV15
Q9F3T0
Q9I5J3
Q9I5J3
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1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tuman:*
5: sp_tunvertebrate:*
5: sp_mammal:*
5: sp_mhc:*
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Q9AXA8
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Q9F189
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Q9KFW3
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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Match 1
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Database :

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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Santos-martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
Mature 407:508 13(2000).
Mature 407:508 123(2000).
EMBL, AL45063; CAC11420.1; -.
InterPro; IPR000914; SBP_bac_5.
Pfam, PF00496; SBP_bac_5.
Pfam, PF00496; SBP_bac_5?
Flam, PF00496; SBP_bac_5?
Flam, PF00496; SBP_bac_5?
Flam, F00496; SBP_bac_5?
Flam, F004060; SBP_bac_5?
Flam, F004060; SBP_bac_5?
Flam, F004060; SBP_bac_5?
Flam, F004060; SBP_BAC_5.
                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE; Sasaki T., Matsumoto T., Yamamoto K.; Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0501G01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.6%; Score 44; DB 17; Length 716; 71.4%; Pred. No. 68; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
NCBI_TaxID=2303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002819; BAB21080.1; -
SEQUENCE 198 AA; 21475 MW; 13F337BABDB9BEFO CRC64;
                                                                                                                                                                                                ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
P0501G01.9 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 44; DB 10;
Similarity 85.7%; Pred. No. 18;
6; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 6; Conserv
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214 GHWGKGEW 221
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabata A., Hikiji T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Okitani R., Ota T., Suzuki Y., Isogai T., Sugano S.; Tanaka T., Nakamura Y., Isogai T., Sugano S.; Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK027045; BAB15636.1; -
InterPro; IPR000810; BTB_POZ.

InterPro; IPR000821; Inf_C2H2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28.4317.4331(2000).

EMBL: APO01508; BAB040771.; -
InterPro; IPR003818; SCFA_trans.

Pfan; PF02667; SCFA_trans; 1.

Complete proteon.

EQUIPMED 441 AA; 47239 MW; 5387892F64302026 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.3%; Score 45; DB 16; Length 441; Best Local Similarity 71.4%; Pred. No. 29; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h Similarity 75.0%; Pred. No. 38; 6; Conservative 1; Mismatches 1; Indels
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SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS50097; BTB; 1.
PROSITE; PS501097; ZINC_FINGER_C2H2_1; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 574 AA; 61827 MW; 28C2FF4DB6C44036 CRC64;
                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SHORT-CHAIN FATTY ACIDS TRANSPORTER.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FL23392 FIS, CLONE HEP17418.
                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=86665;
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                                                                                                                                                                                                       Bacillus halodurans.
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Best Local Similarity
Matches 6; Conserv
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Length 277;

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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Broo S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connetron I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kunita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Media N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schoeb S., Rose M., Sactor P., Sakiuchi J., Sekowska A., Seros B., Rose M., Takemaru K.,
RA Scorokin A., Tamakoshi A., Tanamanch M., Vannier F., Vassarotti A.,
RA Wilari A., Wambutt R., Waller E., Wedler F., Vassarotti A.,
RA Wilari A., Wambutt R., Wammoto H., Vannane K., Vasumoto K., Yata K.,
RA Viari A., Wambutt R., Wammoto H., Vannane K., Pasumoto K., Yata K.,
RY Voshida K., Yoshikawa H.F., Zumstein E., Voshikawa H., Danchin A.;
Rubills.,
RTH complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich D.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF001665; AABB1166.1;
EMBL: AF015775; AAB72056.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99F58EA2F0F36A43 CRC64;
                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus
                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                or oan-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08, VOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9194 MW;
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                                           PRELIMINARY;
                                                                              01-JAN-1998 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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STRAIN-ANCC 15692 / PAO1;
STRAIN-ANCC 15692 / PAO1;
MEDLINE-2043737; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20576172; pubMed=11133964; Sartes C.M., Teixeira M.; Santana M., Pereira M.M., Ellas N.P., Soares C.M., Teixeira M.; Gene cluster of rhodothermus marinus high-potential iron-sulfur protein:oxygen oxidoreductase, a caa3-type oxidase belonging to the superfamily of heme-Copper Oxidases."; J. Bacteriol. 183:687-699(2001).

EMBL, AJ249578; CAC08530.1; -..
      1;
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                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 187;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen.";
Nature 406:959-964(2000).
BEBL: AEGO4892: AAG08179.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 187 AA; 21281 MW; 8908E9EBEE51897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; CFB group; Rhodothermus group; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73CF0EF4970E1E7A CRC64;
                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHERICAL 31.4 KDA PROTEIN.
Rhodothermus marinus (Rhodothermus obamensis).
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                                                                                                                                    187 AA.
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Pred. No. 20;
0; Mismatches
    Mismatches
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Q9HV15;
Q9HV15;
Q1-MAR-2001 (TrEMBLrel. 16, Cr
Q1-MAR-2001 (TrEMBLrel. 16, La
Q1-OCT-2001 (TrEMBLrel. 18, La
HYPOTHETICAL PROTEIN PA4793,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31355 MW;
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87.5%;
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7; Conservative
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                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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277 AA; 3:
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Best Local Similarity
Matches 7; Conserv
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                                              53 GYWG-GYW 59
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                              1 gywgkgyw 8
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SEQUENCE 27
                                                                                                                                                                                                                                                                  Pseudomonas
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DNA Res. 6:83-101(1999).
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99310339; PubMed=10382966; Kawarabayasi Y., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Magai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kubilda N., Ogori A., Aoki K. II., Kubota K., Makamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic
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             Gaps
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pred. No. 46;
0; Mismatches 2; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 358 AA; 40019 MW; 035673ABE6EDDA58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 51.1 KDA PROTEIN APE1820.
                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA0736.
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0
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           Mismatches
  Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
             2;
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EMBL; AE004508; AAG04125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               72.9%;
75.0%;
 71.48;
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Best Local Similarity 75.0.
             5; Conservative
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                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 GTWGGGYW 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum.
NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gywgkgyw 8
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                                   2 ywgkgyw 8
                                                         3 WWGKGWW 9
                                                                                                                                                                                                                     Pseudomonas.
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                                                                                                                           0915J3;
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Q9YAX5
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RATEALER FORTER LEW.

RATEALER PERFELEX;

RAMEDIAGE TO COLINER S.E., Toll R.A., Evans C.A., Gocayne J.D.,

RAMEDIAGE 2019 GOGO, Submed=10731132;

RAMEDIAGE 2019 GOGO, Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Ragers Y. H.C., Blaze; R.G., Champer M., Pfeliffer B.D.,

RA ADTI J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA ADTI J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA ADTI J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballos B.V., Barnan B.P., Bhandari D., Bolshakov S.,

RA Borkwa D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,

RA Borkwa D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Borkwa D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Borkwa D., Botchan A., Deng Z., Mays A.D., Davies P.,

RA Borlos K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Iboywan C.,

RA Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Iboywan C.,

RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kenison J.A., Mackion D.K.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Rainmel B.E., Kodira C.D., Karfet C., McIrod W.P., Morter B.,

Rainer K., Satunder R.A., Worder S., Worter E., Shen H.,

RAIner K., Satunder S., Woller E., Wang A., Wang S., Yang S., Zhan M., Zhang G., Zhan M., Zhang G., Zhan M., Zhang G., Zhan M., Zhang G., Zhan R., Zhang H., Zhang H., Zhang Y., Yen R., Rahner R., Yen R., Randrich M., Shang S., Zhan 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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0
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Pred. No. 62;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                27CA636B23A7FF7B CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                        al protein; Complete proteome.
470 AA; 51138 MW; 27CA636B2
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EMBL, AP000062; BAA80823.1; -.
InterPro; IPR000471; BCl_2.
InterPro; IPR00047; FAD_Gly3P_dh.
InterPro; IPR0004205, NAD_binding.
PRINTS; PR01001; FADG3PDH.
PROSITE; PS01288; BHZ; I.
PROSITE; PS01288; BHZ; I.
SEQUENCE 470 AA; 51138 MW; 27CA6
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 5; Conserv
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102 YWGKGY 107
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                          Horikoshi K.;
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Horikoshi K.;
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Q9F189;
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Matches
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                       RA RT RT DR DR DR KW KW
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MEDLINE-9804537; Pubmed-9383189;
Chandry P.S., Moore S.C., Boyce J.D., Davidson B.E., Hillier A.J.;
"Analysis of the DNA sequence, gene expression, origin of replication and modular structure of the Lactococcus lactis lytic bacteriophage
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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EMBL, AF011378; AAB70078.1; --
Hypothetical protein.
SEQUENCE 133 AA; 15682 MW; 7D985B5C5IE961BC CRC64;
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SEQUENCE FROM N.A.
STRAINS-(125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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0
                                                                                                                                                                                                                                                              71.2%; Score 42; DB 5; Length 126; 71.4%; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                            2; Indels
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL, SAD5105602; AAF51986.1; -
FlyBase; FBgn0037352; CG14673.
SEQUENCE 126 AA; 14140 MW; DC68AB3DF1F5F820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 15.7 KDA PROTEIN.
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Last annotation update)
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NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AA.
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                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.2%; Score 42; DB 100.0%; Pred. No. 23; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.40,
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         37 YWNSGYW 43
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Q9KDB3
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.", Mucleic Acids Res. 28:4317-4331(2000).

EMBL, APO01511; BAB050019.1. - .

InterPro; IPR000182; Acetyltransf_GCN5.
Pfam, PF00583; Acetyltransf_1.

Complete proteome.

SEQUENCE 180 AA; 20375 MW; 100D7285E880BCEB CRC64;
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EMBL; APO01514; BABD5840.1; ...
InterPro; IPR000182; Acetyltransf_GCN5.
Pfam; PF00583; Acetyltransf; 1.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                    71.2%; Score 42; DB 16; Length 180; 100.0%; Pred. No. 32; tive 0; Mismatches 0; Indels
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                           Query Match
Best Local Similarity
6; Conserve
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SEQUENCE FROM N.A.
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SEQUENCE 181 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VENHOEIJEN, Martine Elisa
APPLICANT: VENHOEIJEN, Martine Elisa
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: A MITBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIT: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS DOS TEXT
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
US-08-399-611A-30

US-08-491-334A-30

US-09-077-442-27

US-09-08-08-444A-27

US-09-08-98-47

US-09-08-98-47

US-08-759-628-4

US-08-759-628-4

US-08-759-628-10

US-08-759-628-10

US-08-445-586-10

US-08-446-494-13

US-08-446-13

US-08-446-13

US-08-446-13

US-08-147-623-11

US-09-147-623-11

US-09-147-623-11

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US-09-147-623-11

US-08-147-623-11

US-08-147-623-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. STREET: 9th Floor, East Tower STREET: 9th Floor, D.C. STATE: COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB Pred. No. 24; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: October 16, 1995
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EB/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08860174A Patent No. 5989830 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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amino acid
   MOLECULE TYPE: protein
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Sequence 12, Appl
Sequence 12, Appl
Sequence 27, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 99, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
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9.123 Million cell updates/sec
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.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-860-174A-12

US-08-947-965-78

US-08-469-202-27

US-08-469-202-28

US-08-484-434C-34

US-08-484-434C-34

US-08-484-434C-34

US-08-484-434C-35

US-08-484-434C-35

US-08-423-441-2

US-08-128-131-99

US-08-128-131-99

US-08-128-131-99

US-08-128-131-99

US-08-128-128-22

US-08-128-128-22

US-08-128-131-99

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US-08-128-128-128-128-128-13

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US-08-128-128-13
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Maximum Match 100%
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APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkhuizen, Bauke
APPLICANT: Dijkhuizen, Garsten
APPLICANT: Addersen, Carsten
APPLICANT: Osten, Claus von der
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase;
TITLE OF INVENTION: Variants
FILE REFERENCE: 4285.204-US
CURRENT FILINO NUMBER: US/08/947,965A
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 1173/95
EARLIER APPLICATION NUMBER: 1173/95
EARLIER FILING DATE: 1995-10-17
EARLIER APPLICATION NUMBER: 1281/95
EARLIER APPLICATION NUMBER: PCT/DK96/00179
EARLIER APPLICATION NUMBER: PCT/DK96/00179
EARLIER APPLICATION NUMBER: PCT/DK96/00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.8%; Score 40; DB 2; Length 282; 75.0%; Pred. No. 45;
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CRARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 78
                                                                                                                              APPLICATION NUMBER: US/08/860,174A FILING DATE: June 16, 1997
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US-08-947-9655-78
; Sequence 78, Application US/08947965A
; Patent No. 6004790
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; Sequence 27, Application US/08469202
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CRGANISM: Klebsiella pneumoniae
US-08-947-965-78
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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91 GYWGRDYF 98
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Pred. No. 44;
2; Mismatches 0; Indels
                                                                                                                                             APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: VERHOEIJEN, ABUTON E BIVALENT
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PILLSBÜRY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM

REDIOM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS TE

SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.(
CURRENT APPLICATION DATA:

APPLICATION DATA:

RILNG DATE: June 16, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95307332.7

FILING DATE: October 16, 1995

APPLICATION NUMBER: EP 1995

FILING DATE: AUGUST 16, 1995

FILING DATE: AUGUST 14, 1996

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHRRATERISTICS:

SEQUENCE CHRRATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-860-174A-10; Sequence 10, Application US/08860174A; Patent No. 5989830
                                                                            Sequence 12, Application US/08860174A
Patent No. 5989830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.8%;
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COUNTRY: UNITED STATES
ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.8
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-860-174A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                   GENERAL INFORMATION:
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                                                       US-08-860-174A-12
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LENGTH:

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STATE:

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COMPUTER TEACHER
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBW PC
COMPUTER: IBW PC
COMPUTER: IBW PC
COMPUTER: DATE: Windows NT 4.0; MS Word for Windows 7.0a
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,434C
FILING DATE: 07-UIN-1995
CLASSIFICATION NUMBER: 08/016,881
FILING DATE: 11-FEB-1993
CLASSIFICATION NUMBER: 0800
ATTORNEY/AGENT INFORMATION:
NAME: Schwedler, Carl J.
REGISTRATION NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/08484434C
Patent No. 596914
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene LLC
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 655;
Pred. No. 1.4e+02;
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COMPUTER: Apple Macintosh
OPERATING SYGTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/469,202
FILING DATE: 6-JUNE-95
CLASSIFTCATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 11.FEB_1993
CLASSIFTCATION BOATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 11.FEB_1993
CLASSIFTCATION NUMBER: 31,845
NAME: Blizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Carl J. Scherer
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
REFERENCE/JOCKET NUMBER: 36,924
REFE
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62.58;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.1
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-469-202-28
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STATE:
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   Patent No. 5750875
GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28 Application US/08469202
Patent No. 5750875
GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALGENE, INC.
STREET: 1920 FIFTH STREET
CITY: DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.1%; Score 39; DB 1; Length 655; 62.5%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,202
FILING DATE: 6-JUNE-95
CLASSIFCATION NUMBER: 08/016,881
FILING DATE: 11 FEB 1993
CLASSIFCATION NUMBER: 34,719
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: USA
CAUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
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linear
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Best Local Similarity
Matches 5; Conserv
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122 GYWGRDYF 129
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CITY: DAVIS
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; HYPOTHETICAL:
US-08-469-202-27
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US-08-469-202-28
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Gaps

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GENERAL INFORMATION:

APPLICANT: MAAT, JAN

APPLICANT: MAAT, JAN

APPLICANT: STAM, HEIN

APPLICANT: STAM, HEIN

APPLICANT: STAM, HEIN

APPLICANT: STAM, HEIN

APPLICANT: VAN DE VONDERVORT, PETER J.

APPLICANT: VAN DE VONDERVORT, PETER J.

APPLICANT: VERBAKEL, JOHANNES M.

TITLE OF INVENTION: RIPENING FORM OF A POLYPEPTIDE HAVING SULFHYDRYL OXIDASE

TITLE OF INVENTION: ACTIVITY

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
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APPLICANT: BUSSEY, HOWARD, BOONE, CHARLES; SOMMER, STEVE S.;
HILL, KATHRYN, MEADEM, PHILIP
HILL, ATHRYN, MEADEM, PHILIP
TITLE OF INVENTION: GENES WHICH PARTICIPATE IN B-GLUCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1; Length 392;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
GOMPOTER: IBM FO Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/423,441
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16773
HER: 202744/T7019(V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: CUSHMAN, DARBY & CUSHMAN 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,620
FILING DATE: 09-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTORNAL TRUNCATION NUMBER: 16773 REGISTRATION NUMBER: 16773 REFERENCE/DOCKET NUMBER: 2027 TELECOMMUNICATION INFORMATION: 202-82-934 TELERAX: 202-822-9944 TELEX: 2484530USH FOR SEQ ID NO: 2: SEQUENCE CHRACTERISTICS: LENGTH: 392 amino acids
                                                                                                                                                                                                                                              Sequence 2, Application US/08423441 Patent No. 5529926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 64.4%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 20005
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122 GYWGRDYF 129
                                1 gywgkgyw 8
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                                                                                                                                                                                                                 US-08-423-441-2
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TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene LLC
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.1%; Score 39; DB 2; Length 655; Best Local Similarity 62.5%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 39; DB 2; Length 655; 62.5%; Pred. No. 1.4e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15593/01
REFERENCE/DOCKET NUMBER: 15593/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 530-792-2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/08484434C Patent No. 5969214 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFTCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 11-FEB-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 1559
TELECOMMUNICATION INFORMATION:
TELECHONE: 530-792-2265
TELEFAX: 530-792-2463
                                                                                     INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: LENGTH: 655 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 35:
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LENGTH: 655 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.59
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein; HYPOTHETICAL: NO US-08-484-434C-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GYWGRDYF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gywgkgyw 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Davi
STATE: CA
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US-08-484-434C-35
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.37
5. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-865-99

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                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                          Sequence 99, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                         Score 38; DB 6; Length 1365;
Pred. No. 3.9e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.7%; Score 37; DB 1; Length 29; 83.3%; Pred. No. 15; 0; Indels:ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,316
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 29 amino acids TYPE: AMINO ACID
                                                                                                                                                                     64.4%;
62.5%;
                                                                                                                                                                    Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
; ASSEMBLY AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                           1 gywgkgyw 8
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                                                                                ; SEQ ID NO:4:
; LENGTH: 1365
5194600-4
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US-07-853-408B-99
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US-08-308-865-99
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0
Sequence 99, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 296, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 29;
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                                                                                                                                                                                                                           ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
STREET: Can Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2;
Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14643-9-1-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: WO PCT/US97/21803
ATTORNEY/AGENT INFORMATION:
                                                                                                                                APPLICATION NUMBER: US/09/042,353
FILING DATE: 13 MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
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FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,429
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TELEFRX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 296:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-OCT-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-042-353-296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Gaps AL INFORMATION.
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies ö NUMBER OF SEQUENCES: 417

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
COUNTR: USA
AIT: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SCHWARE: PAtentin Release #1.0, Version #1.30 Score 37; DB 4; Length 29; Pred. No. 15; 1; Mismatches 0; Indels . ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION CURROWN>
PRIOR APPLICATION NUMBER: US 08/728,463
APPLICATION NUMBER: US 08/728,463
APPLICATION NUMBER: US 08/728,463
APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/35,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 00-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 00-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: US 08/155,301 FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APF-1993
APPLICATION NUMBER: US 08/0590,860
FILING DATE: 16-DEC-1992 TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 144; Sequence 144, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION: TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300 TYPE: amino acid STRANDEDNESS: <Unknown> INFORMATION FOR SEQ ID NO: 144: SEQUENCE CHARACTERISTICS: 62.7%; 83.3%; Conservative Best_Local Similarity Matches 5; Conserv 13 GYWGQG 18 1 gywgkg 6 RESULT 14 US-08-758-417A-144 US-08-758-417A-144 Query Match δλ qq

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Job time: 197 sec
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                                                             Gaps
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                                                                                                                                                                                                 RESULT 15
US-08-053-131-99
; Sequence 99, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION:
; TITLE OF INVENTION: Producing Heterologous Antibodies
; TITLE OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
                                                           0;
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0
           62.7%; Score 37; DB 4; Length 29; 83.3%; Pred. No. 15; 0; Indels Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER LUSA

CUDNITY: USA

CUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,131

FILING DATE: 26-APR-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/810,279

FILING DATE: 17-DEC-1991

APPLICATION NUMBER: US 07/810,279

FILING DATE: 18-MRR-1992

ATTORNEY AGENT INFORMATION:

NAME: SMith, William M.

REGISTRATION NUMBER: 14643-9-3

FELECOMMUNICATION INFORMATION:

TELEPHONE: 145-36-2400

TELEPHONE: A15-36-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 30 amino acids TYPE: amino acid
           Query Match 62.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-99
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Search completed: August 12, 2002, 17:22:10

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Compugen Ltd.
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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OM protein - protein search, using sw model

August 12, 2002, 17:22:44; Search time 27.08 Seconds (without alignments) 28.387 Million cell updates/sec Run on:

1 cywgcgyw 8 10-071247-2 66 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES æ

	Description	saposin precursor	hypothetical prote		м	relaxin B,C and A	hypothetical prote	_	hypothetical prote	N-acetylgalactosam	N-acetylgalactosam	probable glycogen	hypothetical prote	late embryogenesis	integral membrane				muscarinic acetylc	hypothetical prote	hypothetical prote	polyprotein - marm		hypothetical prote	hypothetical prote		probable phosphoes	short-chain fatty	n-acetylglucosamin	hypothetical prote
SUMMARIES	ID	A28716	E96704	H84430	A49739	4705	T31757	3175	3175	154210	4	D70770	B72392	G84839	89696н	B29514	A29476	S01114	847572	AF1810	S73827	T08839	PH1663	A69894	T44809	T04561	H86204	F83694	T40367	T36462
	DB	!	~																											
	Length	554	269	283	48	143	342	347	351	473	533	863	83	280	441	589	589	290	590	290	741	2970	113	130	130	396	415	441	456	499
ø	Query Match	69.7	68.89	6.89									62.1		62.1														9.09	•
	Score	46	2	45.5	42		42		42	42	42	42	41	41	41	41	41	41	41	41	41	41	40	40	40	40			40	40
	esult No.	-	7	e	4	S	9	7	æ	6	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	53

saposin precursor	saposin precursor	INDAl protein - fu	angiotensin-conver	major high-(glycin	hypothetical prote	conserved hypothet	probable dCTP deam	probable phosphoes	nitrogenase (EC 1.	hypothetical prote	oxidoreductase (EC	inositol-1,4-bisph	hypothetical prote	nitrogenase (EC 1.	nitrogenase molybd
SAHUP	JH0604	S33212	JC5374	KRSHI6	H84004	A69846	H72759	G83242	S50136	T38935	AF3304	A39254	T05664	NIAIMA	AF1986
-	Н	-	~	Н	~	Н	7	7	~	7	7	~	7	, 	7
527	557	573	630	62	116	118	163	270	304	317	332	400	466	480	497
9.09	9.09	9.09	9.09	8.69	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1
40	40	40	40	39.5	39	39	39	39	39	39	39	39	39	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

- T	17

saposin precursor - rat N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon ein (SAP): sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulf N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

Accession: A28746

R.Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.

B.Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.

B.Rosence number: A28716; MUD:89000647

A.Rosesion: A28716

A.Rosesion: A28716

A.Rosesion: B.RNA

A.Rosesion: B.RNA

A.Rosesreferences: GB.M19936; NID:g206904; PIDN:AAA42136.1; PID:g206905

A.Kote: parts of this sequence, including the amino end of the mature protein, were d

C;Function:
A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them
A;Pathway: sphingolipid catabolism
A;Description: A;Note: saposins A and C (SAP-2) activate hydrolysis of galactocarebroside by beta-gluc
A;Note: saposin B (SAP-1) activates hydrolysis of galactocarebroside sulfate by aryls
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiest
C;Superfamily: saposin repeat homology
C;Keywords: alternative splicing; glycoprotelin; lysosomal storage disease; lysosome;
F;1-16/Domain: signal sequence #status predicted <SIG>F;1-16/Domain: saposin repeat homology <SAPI>F;18-28/Domain: saposin repeat homology <SAPI>F;18-28/Domain: saposin repeat homology <SAPI>F;194-273/Product: saposin repeat homology <SAPI>F;194-273/Product: saposin repeat homology <SAPI>F;310-397/Domain: saposin repeat homology <SAPI>F;310-397/Domain: saposin repeat homology <SAPI>F;311-389/Product: saposin P #status predicted <SAPI>F;311-389/Product: saposin D #status predicted <SAPI>F;311-389/Product: saposin Cepat homology <SAPI>F;311-389/Product: saposin Cepat homology <SAPI>F;311-31,445/Baiding site: carbohydrate (Asn) (covalent) #status predicted F;80.214,331,455/Baiding site: carbohydrate (Asn) (covalent) #status predicted F;80.214,331,455/Baiding site: carbohydrate (Asn) (covalent) #status predicted F;197-270,200-264,229-240,314-331,375/Bisulfide bonds: #status predicted

Gaps ; 0 Score 46; DB 1; Length 554; Pred. No. 17; 2; Mismatches 2; Indels 0; 69.7%; 75.0%; Query Match
Best Local Similarity 75.0
Matches 6; Conservative

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RESULT E96704

a

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A; Map position: 5
A; Introns: 66/3; 122/2; 167/2; 214/3; 319/1
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CYWGC 142
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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Species: Arabidopsis thallana (mouse-ear cress)
C; Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: H84430
C; Accession: H84430
C; Accession: H84430
M; Koo, H; Moffat, K.S; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D; Nierman W.C; White, O.; Elsen, J.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
A; Tile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
A; Reference number: A84420; MUID:20083487
                                                                                                                R:Theologis, A: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jen, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
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A; Molecule type: DNA
A; Residues: 1-283 <STO>
A; Cross_references: GB:AE002093; NID:g6598329; PIDN:AAF18588.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: E96704
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: SNA
A;Residues: 1-269 <STO>
A;Cross-references: GB:AE005173; NID:g6553884; PIDN:AAF16550.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Species: D7-Apr-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: B49739; A49739; A49739
E;Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R.
Endocrinology 129, 375-383, 1991
hypothetical protein T23K23.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5; DE
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.9%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 68.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 CYRWGCGGW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 CYRWGCGGW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 cy-wgcgyw 8
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A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: T23K23.3
A;Map position: 1
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A; Title: Affinity purification and sequence determination of equine relaxin.

A; Reference number: A49739; MUID:91275796

A; Accession: B49739

A; Molecule type: protein
A; Molecule type: pyroglutamic acid
C; Superfamily: insulin
A; Residues: 29-48 cST2>
C; Superfamily: insulin
A; Residues: 29-48 pyroglutamic acid
F: 1-28/Domain: chain B #status experimental <MAT>
F: 12-24 B/Domain: chain A #status experimental <CHA>
F: 12-24 B/Domain: chain A #status experimental <CHA>
F: 12-24 B/Domain: chain B #status experimental <CHA>
F: 12-39,35-48/Disulfide bonds: #status pyredicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Equus sp.
C; Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 16-Jul-1999
C; Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 16-Jul-1999
C; Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 16-Jul-1999
C; Accession: 147053
B; Klonisch, T.; Ryan, P.L.; Yamashiro, S.; Porter, D.G.
B; R; Rionisch, T.; Ryan, P.L.; Yamashiro, S.; Porter, D.G.
B; R; Rionisch, T.; Ryan, P.L.; Yamashiro, S.; Porter, D.G.
A; Title: Partial complementary decxyribonucleic acid cloning of equine relaxin messen
A; Reference number: 147053
A; MUD:95359320
A; Accession: 147053
A; Residues: 1-143
A; Modelues: 1-143
A; Modelues: 1-143
A; Modelues: 1-143
A; Cross-references: GB:S78800; NID:91042059; PIDN:AAB35036.1; PID:91042060
C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C07G3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oscaria 1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C;Accession: T31757
R;Geisel, C.; Wamsley, P.
R;Reference number: Z21080
A;Reference number: Z21080
A;Reference number: Z21080
A;Residues: 1-342 - GGEI>
A;Residues: BmBL:AFO16432; PIDN:AAB65382.1; GSPDB:GN00023; CESP:C07G3.4
A;Residues: Strain Bristol N2; clone C07G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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9.6;
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100.0%; Pred. No. 22;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.6%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 9.6 Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relaxin B, C and A chains - horse (fragment)
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hypothetical protein C07G3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Co-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C:Accession: T31758
R:Geisel, C.; Wamsley, P.
Submitted to the RMLD Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C07G3.
A:Reference number: 221080
A:Reference number: 221080
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1.351 GEI>
A:Genello CSS - references: EMBL:AF016432; PIDN:AAB65377.1; GSPDB:GN00023; CESP:C07G3.3
A:Experimental source: strain Bristol N2; clone C07G3
A:Genellos: A:Genellos: 5
A:Map position: 5
A:Introns: 66/3; 122/2; 167/2; 214/3; 319/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross references: EMBL:AF016432; PIDN:AAB65378.1; GSPDB:GN00023; CESP:C07G3.6
A:Experimental source: strain Bristol N2; clone C07G3
C:Genetics:
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                                                                                                                                                                                                                         hypothetical protein C07G3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cact-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31755
R;Geisel, C.; Wamsley, P.
Submitted to the EMBL Data Library, July 1997
A;Bescription: The sequence of C. elegans cosmid C07G3.
A;Reference number: 221080
A;Accession: T31755
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-347 <GEL>
                                                           Gaps
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                  DB 2;
                Score 42; DB 2,
Pred. No. 44;
0; Mismatches
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A;Introns: 66/3; 122/2; 167/2; 214/3; 319/1
63.6%; Scor.
100.0%; Pre
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Thes 5; Conserve
              Query Match
Best Local Similarity
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Matches 5; Conserv
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A.Title: Micopolysaccharidosis type VI in rats: Isolation of cDNAs encoding arylsulfa A;Reference number: 154210; MUID:96121368
A;Accession: 154210
A;Accession: 154210
A;Accession: 154210
A;Accession: 154210
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-473 <RES>
A;Cross-references: GB:D49434; NID:91065603; FIDN:BAA08412.1; PID:91089794
C;Genetics:
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A; Residues: 1-533 cpp:
A; Rodacest, S.; Rupp, K.; von Figura, K.; Peters, C.
Cross-references: EMBL:X72735; NID:9289009; PIDN:CAA51272.1; PID:9825628
R; Modaresst, S.; Rupp, K.; von Figura, K.; Peters, C.
Biol. Chem. Hoppe-Seyler 374, 327-335, 1993
A; Title: Structure of the human arylsulfatase B gene.
A; Reference number: S33307; MUD:93332648
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-104 cMOD>
A; Cross-references: EMBL:X72735; EMBL:X72736; EMBL:X72739; EMBL:X72739; A; Note: the anzyme is referred to as EC 3.1.6.9
B; Peters, C.; Schmidt, B.; Rommerskirch, W.; Rupp, K.; Zuehlsdorf, M.; Vingron, M.; M.; Hiol. Chem. 265, 3374-3381, 1990
A; Title: Phylogenetic conservation of arylsulfatases. CDNA cloning and expression of A; Accession: A35078; MUD:90153994
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A. Residues: 1-357, 'V' 359-533 <PBZ>
A. Cross-references: GB.J05225; NID:q179076; PIDN:AAA51784.1; PID:q179077
A. Mote: parts of this sequence were determined by protein sequencing
A. Note: the enzyme is referred to as EC 3.1.6.1
A. Note: the enzyme is referred to S. C. P.; Gibson, G.J.; Beckmann, K.R.; Hopwood, J.J.
B. Lochem. Int. 24, 209-215, 1991
A. Title: Human N-acetylgalactosamine-4-sulphatase: protein maturation and isolation o
A. Reference number: A45659; MUID:92028992
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N-acetylgalactosamine-4-sulfatase (EC 3.1.6.12) precursor - rat (fragment) Nichternate names: arylsulfatase (EC 3.1.6.1) B [misidentification] C.Species: Rattus norvegicus (Norway rat) (C.Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 02-Jun-2000 C.Accession: I54210 (C.Accession T.A.B.) Rikmieda, T. Genomics 29, 582-587, 1995
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56;
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Best Local Similarity
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Cincession: D70770
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Bavies, R.; Pevilla, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; Mulb:98295987
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-863 <COL>
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                           probable glycogen phosphorylase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Pred. No. 89;
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Nature 399, 323-329, 1999
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A; Residues: 1-83 <ARN>
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A;Gene: TM0315
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A;Residues: 403-404, Y', 406-407 <JIS>
A;Molecule type: mRNA
A;Residues: 403-404, Y', 406-407 <JIS>
A;Residues: 403-404, Y', 406-407 <JIS>
A;Rolecule type: mRNA
A;Residues: 403-404, Y', 406-407 <JIS>
A;Rolecule type: mRNA
A;Residues: 403-404, Y', 406-407 <JIS
A;Note: the enzyme is referred to as EC 3.1.6.1
A;Note: the enzyme is referred to as EC 3.1.6.1
A;Note: the enzyme is referred to mucopolysaccharidosis type VI, Maroteaux-Lamy disea
A;Note: these mutations give rise to mucopolysaccharidosis type VI, Maroteaux-Lamy disea
R;Schmidt, B.; Selmer, T.; Ingendoh, A.; von Figura, K.
Cell 82, 271-278, 1995
A;Title: A novel amino acid modification in sulfatases that is defective in multiple sul
A;Reference number: A57113; MUID:95354208
A;Contents: annotation; identification of 3-oxoalanine, 2-amino-3-oxopropanoic acid
R;Schuchman, E.H.; Jackson, C.E.; Desnick, R.J.
Genomics 6, 149-158, 1990
A;Title: Human arylsulfatase B: MOPAC cloning, nucleotide sequence of a full-length cDNP
A;Reference number: 154217; MUID:90152677
A;Reture: preliminary; translated from GB/EMBL/DDBJ
A;Reture: preliminary;
A;Rolecule type: mRNA
A;Recession: 1357, VV, 377-533 <RES>
A;Cross-references: GB:M32373; NID:9179029; PIDN:AAA51779.1; PID:9179030
B;Robayashi, T.; Honke, K.; Jin, T.; Gasa, S.; Miyazaki, T.; Makita, A.
B;Robayashi, T.; Honke, R.; Jin, T.; Gasa, S.; Miyazaki, T.; Makita, A.
A;Title: Components and proteolytic processing sites of arylsulfatase B from human place
A;Reference number: A56865; MUID:93003385
A;Cross-referencesion: A56865
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A;Map position: 5q11-5q13
A;Introns: 104/3; 167/1; 230/3; 300/1; 381/2; 405/1; 446/1
A;Note: defects in this gene can cause mucopolysaccharidosis type VI, Maroteaux-Lamy dis C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Superciption: hydrolyzes N-acetylgalactosamine-4-sulfate units in chondroitin sulfate a Superfamily: animal sulfatase (Superfamily: animal sequence #status predicted <SIG>
F;41-423/Product: alpha chain #status predicted <AMAT>
F;424-465/Product: gamma chain #status predicted <AMAT>
F;466-533/Product: beta chain #status experimental <BRAT>
F;188-279,536,458/Bainding site: carbohydrate (Asn) (covalent) #status predicted
F;291/Bainding site: carbohydrate (Asn) (covalent) #status absent
F;426/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                      dete
50 an
A; Note: sequence extracted from NCBI backbone (NCBIN:57777, NCBIP:57778)
A;Note: the enzyme is referred to as EC 3.1.6.1
A;Note: parts of this sequence, including the amino end of the mature protein, were detered; a form is described with a proteolytic cleavage somewhere between residue 450 an R;Jin, W.D.; Jackson, C.E.; Desnick, R.J.; Schuchman, E.H.
Am. J. Hum. Genet. 50, 795-800, 1992
A;Title: Mucopolysaccharidosis type VI: identification of three mutations in the arylsul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Kesidues: 41-155,424-425, x7,427-454;466-483 < KOB>
A. Kesperimental source: placenta A. Kesperimental source: placenta A. Note: sequence modified after extraction from NCBI backbone A. Note: the fragments shown are the amino ends of the alpha, gamma, and beta chains of C. Comment: This enzyme is frequently misidentified as EC 3.1.6.1.
                                                                                                                                                                                                                                                                                            A;Reference number: A42449; MUID:92197625
A;Accession: A42449
A;Molecule type: mRNA
A;Residues: 115-116, "X, 118 <JIN>
A;Cross-references: GB:S90729; NID:g247486; PIDN:AAB21831.1; PID:g247487
A;Note: sequence extracted from NCBI backbone (NCBIN:90729, NCBIP:90731)
A;Accession: B42449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 234.235, Pr, 237-238 <JI2>
A;Residues: 234.235, Pr, 281.590736; NID:g247488; PIDN:AAB21832.1; PID:g247489
A;Cross-reference: extracted from NCBI backbone (NCBIN:90736, NCBIP:90739)
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62;
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Pred. No.
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85.78;
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A;Cross-references: GB:AE001713; GB:AE000512; NID:g4980809; PIDN:AAD35403.1; PID:g498
A;Experimental source: strain MSB8
C; Accession: B72392
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                 A;Tile: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Accession: B72392
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50.0%; Pred. No. 20;
iive 2; Mismatches
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Best Local Similarity

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Length 863;

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Search completed: August 12, 2002, 17:22:45 Job time: 182 sec
              A; Reference number: A94293; MUID:87263421
                                        A; Accession: B94293
A; Molecule type: mRNA
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A; Status: preliminary
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R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A:Reference number: A96900; MUID:21359325, PMID:21359325

A:Reference number: A96900; MUID:21359325, PMID:21359325

A:Status: preliminary
A:Residues: 1-441 < KUR>
A:Residues: 1-441 < KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78539.1; PID:g15023427; GSPDB:GN00168

A:Genetics:
A:Genetics:
                                                    C;Accession: G84839
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID: 20083487
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Accession: B94518; B94293; B37121; B29514
R; Bonner, T.I.
R; Bonner, T.I.
R; Bonner, T.I.
R; Reference number: A94518
A; Reference number: A94518
A; Reference number: M845
A; Reference number: B94518
A; Residues: 1-589 < B01>
R; Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-522, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 74;
1; Mismatches 1; Indels
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52;
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Pred. No. 52;
1; Mismatches
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60.0%;
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ilarity 71.4%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-280 <STO>
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333 CFWGMGY 339
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A; Residues: 1-269,463-589 <B02>
A; Residues: 1-269,463-589 <B02>
A; Experimental source: cerebral cortex
A; Note: only a part of the protein translation is given; none of the nucleotide seque
B; Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.
J. Biol. Chem. 265, 13702-13708, 1990
A; Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues i
A; Reference number: A37121; MUID:90337982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Molecule type: protein
A. Residues: 104-166 cKUR>
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
F: 67-90/Domain: transmembrane #status predicted <TMA>
F: 104-124/Domain: transmembrane #status predicted <TMA>
F: 184-206/Domain: transmembrane #status predicted <TMA>
F: 184-206/Domain: transmembrane #status predicted <TMA>
F: 180-251/Domain: transmembrane #status predicted <TMA>
F: 425-512/Domain: transmembrane #status predicted <TMA>
F: 527-545/Domain: transmembrane #status predicted <TMA>
F: 527-545/Domain: transmembrane #status predicted <TMA>
F: 5127-545/Domain: transmembrane #status predicted <TMA>
F: 5127
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Pred. No. 93;
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0; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2002, 17:27:25 ; Search time 13:51 Seconds (without alignments) 22:928 Million cell updates/sec Run on:

10-071247-2 66

1 cywgcgyw 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	5 gallus ga	rattus	eduus	rattus	P15848 homo sapien	_	_		P41984 bos taurus	æ	P75443 mycoplasma	~	Ω	E	P34054 trichoderma	_		_	P49441 homo sapien	bos t	7 plas	-	P03385 moloney mur	_	Q9bq08 homo sapien	P74130 synechocyst		Q9j5c7 fowlpox vir			a4 pan t	22	10
SUMMARIES	;	ai T	SAP_CHICK	SAP_RAT	RELX_HORSE	ARSB_RAT	ARSB_HUMAN	PHSG_MYCTU	ACM3_MOUSE	ACM3_RAT	ACM3_BOVIN	ACM3_PIG	YD35_MYCPN	SAP_HUMAN	SAP_BOVIN	SAP_MOUSE	INA1_TRIHA	KR62_SHEEP	NIFD_NOSCO	INPP_MOUSE	INPP_HUMAN	INPP_BOVIN	TBG_PLAFO	NIFD_ANASP	ENV_MLVMO	RSNB_MOUSE	RSNB_HUMAN	TRE2_SYNY3	KRHA_RABIT	V093_FOWPV	ACM3_GORGO	ACM3_HUMAN	ACM3_PANTR	ACM3_PONPY	PUR2_DROME
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ALIGNMENTS

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                   RREAR SEED OF THE SELECT SEED OF THE SEED 
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SAPOSIN LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 3.
SAPOSIN-LIKE TYPE B 4.
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SAPOSIN-LIKE TYPE B 2.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                            SMART; SM00162; SAPA; 2.
SMART; SM00118; SAPB; 4.
Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat;
GM2-gangliosiosis.
SIGNAL
17
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Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> T (IN REF. 2).
-> D (IN REF. 2).
B803000E891C3963 CRC64;
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                EMBL; AB003471; BAA19914.1; -.
EMBL; AF108656; AAF05899.1; -.
InterPro: IPR0000119; SapA.
InterPro: IPR000004; SapB.
InterPro: IPR003259; Saposin.
Probom; PP001732; SAPA; 2.
Probom; Pp001732; SapB; 3.
Probom; Pp001732; SapBi; 1.
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Local Similarity 75.0%;
hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95359320; PubMed=7543295; Klonisch T., Ryan P.L., Yamashiro S., Porter D.G., "Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91275796; PubMed-2055195; Stewart D.R., Nevins B., Hadas E., Vandlen R.; Stewart D.R., Nevins B., Hadas E., Vandlen R.; Stewart D.R., Nevins B., Hadas E., Vandlen R.; Edwart D.R., Nevins B., Hadas E., Vandlen R.; Endocrinology 129:375-383(1991).

-I. FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.

-I. SUBBUILT: HETEROLIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                              DB 1; Length 554;
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-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                 Indels
                                                                                                            DFE3F3A3A0520C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lecular cloning of equine preprorelaxin cDNA."; Reprod. Dev. 42:171-178(1996),
  D -> E (IN REF. 2).
I -> V (IN REF. 3).
W -> R (IN REF. 3).
S -> M (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.2056; 028907; 10. Created) 01-AUG-1991 (Rel. 19, Created) 01-NUG-1997 (Rel. 35, Last sequence update) 10-CCT-2001 (Rel. 40, Last annotation update) Prorelaxin precursor (RXN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AA
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Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                           69.7%; Score 46; 75.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-HOKKAIDO; TISSUE-Placenta;
Min K., Shiota K., Ogawa T.;
"Molecular cloning of equine prep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Reprod. 52:1307-1315(1995).
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                                                                                                               61123 MW;
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PIR; A49739; A49739.
PIR; B49739; B49739.
HSSP; P01348; 4RLX.
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554 AA;
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Best Local Similarity
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ID RELX_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalía; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                         Gaps
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-1- SUBCELLULAR LOCATION: LYSOSOMA1.
-1- DISEASE: DEFECTS IN ARSB ARE THE CAUSE OF MAROTEAUX-LAMY SYNDROME; ALSO KNOWN AS MUCOPOLISACCHARIDOSIS TYPE VI (MPS-VI).
-1- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                              01-0c7-1996 (Rel. 34, Created)
01-0c7-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Arylsulfattase B (EC 3.1.6.12) (ASB) (N-acetylgalactosamine-4-sulfatase) (G4S) (Fragment).
                                                                      COUNECTING PEPPIDE.
RELAXIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
A -> V (IN REF. 2).
L -> Q (IN REF. 2).
W, E5C9414303A838B8 CRC64;
                                                                                                                                                                                                                       63.6%; Score 42; DB 1; Length 182; 100.0%; Pred. No. 6.7; ive 0; Mismatches 0; Indels
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NON_TER 1 1 2-AMINO-3-OXOPROPIONIC ACID
                                                               RELAXIN B CHAIN.
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InterPro: IPR000917; Sulfatase.
Pfam: PF00884; Sulfatase; 1.
PROSITE; PS00523; SULFATASE_1; 1.
PROSITE; PS00149; SULFATASE_2; FALSE_NEG.
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MEDLINE-96121368; PubMed-8575749;
                                Hormone; Signal.
PROSITE; PS00262; INSULIN; 1. Insulin family; Hormone: Sirrary
                                                                                                                                                                               20721 MW;
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156
182
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173
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161
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133
182 AA;
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Best Local Similarity
Matches 5; Conserv
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CONFLICT
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P50430;
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82:271-278(1995)

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MEDDLINE-90152677; PubMed=1968043;
Schuchman E.H., Jackson C.E., Desnick R.J.;
Human arylsulfatase B: MoPAc cloning, nucleotide sequence of a full-length cDNA, and regions of amino acid identity with arylsulfatases A
                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-2000 (Rel. 39, Last annotation update)
Arylsulfatase B precursor (EC 3.1.6.12) (ASB) (N-acetylgalactosamine-4-sulfatase) (G4S).
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95354208; PubMed-7628016; Schmidt B., Selmer T., Ingendoh A., von Flgura K.; A novel amino acid modification in sulfatases that is defective in multiple sulfatase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-92028992; PubMed=1930244;
Litjens T., Morris C.P., Gibson G.J., Beckmann K.R., Hopwood J.J.,
"Human N-acetylgalactosamine-4-sulphatase: protein maturation and
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                 (POTENTIAL).
                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90153994; PubMed=2303452;
Peters C., Schmidt B., Rommerskirch W., Rupp K., Zuehlsdorf M., Vingron M., Meyer H.E., Pohlmann R., von Figura K.;
"Phylogenetic conservation of arylsulfatases. cDNA cloning and expression of human arylsulfatase B.";
J. Biol. Chem. 265:3374-3381(1990).
                                                                                     . .) (POTENTIAL) . .) (POTENTIAL)
                                                                                                        (POTENTIAL)
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                                                                                                                                              Length 473;
                                                                                                                                                                  1; Indels
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N-LINKED (GLCNAC..
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                                                                                                                                             Score 42; DB 1;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AMINO-3-OXOPROPIONIC ACID MODIFICATION SITE.
                                                                                                                                                                                                                                                       533 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolation of genomic clones.";
Biochem. Int. 24:209-215(1991).
                                                                                                                  MW.
                                                                                                                                              63.68;
85.78;
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                                                                                                                  473 AA;
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Best Local Similarity
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92197625; PubMed-1550123;
MEDLINE-92197625; PubMed-1550123;
Jin W.-D., Jackson C.E., Desnick R.J., Schuchman E.H.;
"Mucopolysaccharidosis type VI: identification of three mutations in
the arylsulfatase B gene of patients with the severe and mild
phenotypes provides molecular evidence for genetic heterogeneity.";
Am. J. Hum. Genet. 50:795-800(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92042029; PubMed-1718978; Wicker G., Prill V., Brooks D., Gibson G., Hopwood J., Wicker G., Prill V., Brooks D., Gibson G., Hopwood J., Von Figura K., Peters C.; "Mucopolysaccharidosis VI (Maroteaux-Lamy syndrome). An intermediate clinical phenotype caused by substitution of valine for glycine at position 137 of arylsulfatase B."; Dosttion 266:21386-21391(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Littlens T., Brooks D.A., Peters C., Gibson G.J., Hopwood J.J.;
Lidentification, expression, and biochemical characterization of
acetylgalactosamine-4-sulfatase mutations and relationship with
clinical phenotype in MPS-VI patients.";
Am. J. Hum. Genet. 58:1127-1134(1996).
                          MEDLINE=97184692; PubMed=9032078;
Bond C.S., Clements P.R., Ashby S.J., Collyer C.A., Harrop S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Four novel mutant alleles of the arylsulfatase B gene in two patients with intermediate form of mucopolysaccharidosis VI (Maroteans-Lamy sundrome) ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Voskoboeva E., Isbrandt D., von Figura K., Krasnopolskaya X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS MPS-VI MET-92; GLN-95; CYS-210; PRO-393 AND PRO-498 MEDLINE-96213747; PubMed-8651289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO-3-OXOPROPIONIC ACID.
SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
                                                                                        Hopwood J.J., Guss J.M.; "Structure of a human lysosomal sulfatase."; Structure 5:277-289(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT MPS-VI VAL-137, AND VARIANT MET-376.
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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Hum. Genet. 93:259-264(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                             C -> R (IN MPS-VI; SEVERE FORM).
/FTIG-VAR_007296.
G -> V (IN MPS-VI; INTERMEDIATE FORM).
/FTIG-VAR_007297.
R -> W (IN MPS-VI; INTERMEDIATE FORM).
/FTIG-VAR_007298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R -> Q (IN MPS-VI; INTERMEDIATE FORM).
/FTId=VAR_007299.
Y -> C (IN MPS-VI; MILD/INTERMEDIATE).
                                                                                                                                                                                                                                                                                                                                                                                         R -> Q (IN MPS-VI; MILD/SEVERE FORM). /FIId=VAR_007295.
                                                                                                                                                                 MIM: 2722UU; -.
InterPro: IPR000917; Sulfatase.
Pfam: PF00884; Sulfatase; 1.
PROSITE; PS001523; SULFATASE_1; 1.
PROSITE; PS00199; SULFATASE_2; 1.
Hydrolase; Signal; Glycoprotein; Lysosome; Mucopolysaccharidosis; Disease mutation; Polymorphism; 3D-structure.
SIGNAL 1 36 PARLESULFATASE B.
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L -> P (IN MPS-VI; MILD FORM).
/FTId=VAR_007301.
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C -> Y (IN MPS-VI; MILD FORM).
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V -> M (IN REF. 3).
5983FB6911C4789A CRC64;
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                            EMBL; J05225; AAA51784.1; -.
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533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                 DEVENDENCE ROOM W. N. STRAIN-H37RV;
MEDLINE-98295987; PubMed=9634230;
OLG S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRALM-ECC 1551 / Oshkosh;
STRALM-ECC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whole genome comparison of Mycobacterium tuberculosis clinical and
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Glycogen metabolism; Pyridoxal phosphate; Complete proteome.
BINDING 618 618 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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E39826B03D5B374F CRC64;
                                                                                         (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                   863 AA.
                                                                                                                                                                            Glycogen phosphorylase (EC 2.4.1.1).
GLGP OR RV1328 OR MT1370 OR MTCY130.13.
                                   PRT;
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InterPro; IPR000811; Phosphorylase.
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EMBL, AAE007010; AAK45634.1; -.
HSSP; P06738; 1XGP.
TIGR; MT1370; -.
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                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                   STANDARD;
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                                                                                      01-0CT-1996 (
01-0CT-1996 (
16-0CT-2001 (
                            PHSG_MYCTU
Q10639;
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63.6%; Score 42; DB 1; Length 533; llarity 85.7%; Pred. No. 17; Conservative 0; Mismatches 1; Indels

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"Cultured neurons from mouse brain reproduce the muscarinic receptor profile of their tissue of origin.";
Eur. J. Neurosci. 6:1691-1701(1994).
-i. FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONDES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES, MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88398; Chrm3.
MGD; MGI:88398; Chrm3.
InterPro: 1PR000276; GPCR_Rhodpsn.
PROSTITE; PS000237; GPCRRHODOPSN.
PROSTITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSTITE; PS002637; G_PROTEIN_RECEP_F1_2; 1.
POSTSYNAPLIC membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
DOMAIN 1 66
                                                                                                                                                                                                                                                                                                         Gomeza J., Wess J.; Isolation of mouse muscarinic isolation, sequence and functional expression of mouse muscarinic acetylcholine receptor genes."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                             0;
                   Score 42; DB 1; Length 863; Pred. No. 25;
                                              Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                   ACM3_MOUSE STANDARD; PRT; 589 AA.
09ER23; 064055;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3 (Mm3 mAChR).
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                                             0; Mismatches
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MEDLINE=95179320; PubMed=7874308;
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                                              5; Conservative
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MEDLINE=88077068; PubMed=3120722;
Braun T., Schofield P.R., Shivers B.D., Pritchett D.B., Seeburg P.H.;
"A novel subtype of muscarinic receptor identified by homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                   CYTOPLANTAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furuta M., Ohya S., Imaizumi Y., Watanabe M.; "Molecular cloning of m3 muscarinic acetylcholine receptor in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILIDE-8726321; PubMed-3037705;
Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                              ;
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MEDLINE-92037535; PubMed=1657592;
WESS J., Gdula D., Brann M.R.;
"Site-directed mutagenesis of the m3 muscarinic receptor:
identification of a series of threonine and tyrosine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonner T.I., Young A.C., Brann M.R., Buckley N.J.; "Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor genes.";
                                                                                                                                                                                                                                                                                                                                                 Length 589;
                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                        SIMILARITY. AB782149EBEE7804 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 149:125-132(1987).
                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P08483; Q9QwK9;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
Muscarinic acetylcholine receptor M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 AA
                                                                                                                                                                                                                                                                                                                                                   Score 41; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iris.";
J. Smooth Muscle Res. 34:111-122(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Iris;
MEDLINE=99138467; PubMed=9972520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISION TO 184.
MEDLINE=90166521; PubMed=3272174;
                                                                                                                                                                                                                                                                                     ..
X
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ilarity 71.4%;
Conservative
251
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520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuron 1:403-410(1988)
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
The 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                  GCRDb; GCR_0119; --
GCRDb; GCR_0119; --
GCRDb; GCR_0119; --
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS00245; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PROTEIN_RECEP_FI_1; 1.
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CYDOLASMIC (POTENTIAL).

(CYDOLASMIC (POTENTIAL).

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TO POTENTIAL).

TO POTENTIAL).

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N-LINKED (GLCNAC. ...) (POTENTINED (GLCNAC.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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   involved in agonist but not antagonist binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M16407; AAA40661.1; ALT_SEQ.
EMBL, M16408; AAA40662.1; ALT_SEQ.
EMBL; M18088; AAA40659.1; --
EMBL; M62826; AAA41553.1; --
EMBL, AB017656; BAA36839.1; --
PIR: B29514; B29514
                                                                                                                     MEDLINE=92406875; PubMed=1527051;
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                                EMBO J. 10:3729-3734(1991)
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GCRDb; GCR_0116; -.
GCRDb; GCR_0118; -.
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556
589 AA;
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                                                                                              MUTAGENESIS.
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Length 589;

DB 1; 26;

Score 41; Pred. No.

62.1%; 71.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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GCRDb; GCR_1227; --
InterPro; PRR0021; 7tm_1; 1.
PRINTS; PR00237; GPCRRHDODPSN.
PROSITE; PS502625; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS502625; G_PROTEIN_RECEP_F1_2; 1.
PROSITE PROTEIN_RECEP_F1_2; 1.
PROSITE PROTE
                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee P.H., Hodges P.K., Glickman F., Chang K.J.; "Cloning and expression of a cDNA encoding bovine muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                             (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1223:151-154(1994).
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                                                                                                                                                                                                                                                                 Muscarinic acetylcholine receptor M3
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MEDLINE=94339178; PubMed=8061048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 327-467 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetylcholine m3 receptor
                                                                                                                                                        STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                            524 YWNLGYW 530
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
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2 умдсдум 8
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01-NOV-1995
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                                                                                                                                                   ACM3_BOVIN
P41984;
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Phosphorylation;
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DISULFID
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENTARE CYCLASE, BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY IRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-88296835; PubMed=3402600;
Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.;
"Primary structure of porcine muscarinic acetylcholine receptor III
and antagonist binding studies.";
FEBS Lett. 235:257-261(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam. PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSTIE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
                      CYTOPIASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

F > S (IN REF. 2).

A > G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                         Length 590;
                                                                                                                                                                                                                                                                2; Indels
                                                                                                                         F -> S (IN REF. 2).
A -> G (IN REF. 2).
F -> L (IN REF. 2).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
A DEQUEDE33CCA8D6 CRC64;
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3.
                                                                                                                                                                                                                                                                                                                                                                             590 AA.
                                                                                                                                                                                                                                         Score 41; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S01114; S01114.
GCRDb; GCR_0104; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                 ;
0
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01-OCT-1989 (Rel. 12, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                     ₹.
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                                                                                                                                                                                                                                         62.1%;
71.4%;
                                                                                                                                                                                                     66103
                                                                                                                                                                                                                                          Query Match 62.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                             15
41
48
53
221
424
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461
467
590 AA;
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                                                                                                                                                                                                                                                                                        2 ywgcgyw 8
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                                                                                                                                                                                                                                                                                                                                                                  ACM3_PIG
ID ACM3_PIG
AC P11483;
                                                                                                               DISULFID
CONFLICT
CONFLICT
CONFLICT
              TRANSMEM
DOMAIN
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                                       CARBOHYD
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   DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                    S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.PNEUMONIAE MPN333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
Multigene family, G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1; Length 590;
Pred. No. 26;
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Pfam; PF02932; Neur_chan_memb; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-NR-2002 (Rel. 41, Last annotation update)
Hypothetical protein MPN335 (F10_corf741).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 E
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71.48;
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Best Local Similarity 71.4
Matches 5; Conservative
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                                               Mycoplasma pneumoniae.
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MPN335 OR MP501.
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Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89255151; PubMed=2498298;
Nakano T., Sandhoff K., Stuemper J., Christomanou H., Suzuki K.;
"Structure of full-length cDNA coding for sulfatide activator, a
Co-beta-qlucosidase and two other homologous proteins: two alternate
forms of the sulfatide activator.";
J. Blochem. 105:152-154(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saposin A (Protein A);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Created)
01-APR-1980 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Proactivator polypeptide precursor [Contains: Saposin A (Protein A) Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside Saposin C (Co-beta-glucosidase) (Dispersin) (Sulfatide/GM1 activator);
Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-1); Saposin D (Protein C) (Component C)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      РОТБО2; РОТ292; Р15793; Р78546; Р78547; Q92741; Q92742; Q12740; Q92741; Q92742; Q12742; Q1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The organization of the gene for the human cerebroside sulfate
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                                                                                                                                                                                                                                           POTENTIAL.
1776A96BCF83567F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
    POTENTIAL. POTENTIAL.
                                                                                                                 POTENTIAL. POTENTIAL.
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Pred. No.
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                                                                                 POTENTIAL
                                                                                                                                                                                                  POTENTIAL
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MEDLINE-88068647; PubMed=2825202;
Dewji N.N., Wenger D.A., O'Brien J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90129043; PubMed=2515150;
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                                                                                                                                                                                                                                                                               MM:
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                                                                                                                                                                                                                                                                                                                                                                                            62.1%;
71.4%;
                                                                                                                                                                                                                                                                   85025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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96
140
176
207
675
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Strausberg R.;
                                                                                                                                                                                                                                                                       741 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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SEQUENCE FROM N.A.
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SAP_HOWAN
ID AC P0756]
AC P0756]
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Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J., Waring A.J., To T., Fluharty C.B., Faull K.F., "Preparation of the cerebroside sulfate activator (CSAct or saposin B)
                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Kidney;
MEDLINE-91006165; PubMed-2209618;
Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
"The complete amino-acid sequences of human ganglioside GM2 activator protein and cerebroside sulfate activator protein.";
Eur. J. Biochem. 192:709-714(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89207118; PubMed=3242555; Kleinschmidt T., Christomanou H., Braunitzer G.; "Complete amino-acid sequence of the naturally occurring A2 activator profein for enzymic sphingomyelin degradation: identity to the sulfatide activator protein (SAP-1)."; Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQÜENCE OF 311-390.

MEDLINE-88163077; PubMed=3442600;

RICHINE-88163077; PubMed=3442600;

"Complete amino-acid sequence and carbohydrate content of the naturally occurring glucosylceramide activator protein (Al activator) absent from a new human Gaucher disease variant.";

Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
Nucleotide sequence of cloned cDNA for human sphingolipid activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89000190; PubMed=3048308;
Furst W., Machleidt W., Sandhoff K.;
"The precursor of sulfatide activator protein is processed to three
                                                                                                                                                                                                                                                             Hill F., O'Brien J.S.; "Molecular cloning of the sphingolipid activator protein-1 (SAP-1), the sulfatide sulfatase activator.";
                                                                                                      Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S., Kishimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kondoh K., Hineno T., Sano A., Kakimoto Y.;
"Isolation and characterization of prosaposin from human milk.";
Blochem. Biophys. Res. Commun. 181:286-292(1991).
                                                                                                                                                                                                                                            Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE OF SAPOSIN B, AND STRUCTURE OF CARBOHYDRATES
                                                                                                                                               "Saposin A: second cerebrosidase activator protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89025876; PubMed-2845979;
Morlinoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
Mosposin D: a sphingomyelinase activator.";
Blochem. Biophys. Res. Commun. 156:403-410(1988).
                 protein 1 precursor.";
Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).
                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 134:989-994(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Chem. Hoppe-Seyler 369:317-328(1988).
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STRUCTURE OF CARBOHYDRATE ON ASN-215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genet. Metab. 68:391-403(1999).
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                                                                                                                                                                                                  SEQUENCE OF 195-263 FROM N.A. MEDLINE=86130593; PubMed=2868718;
                                                                                            PubMed=2717620;
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                                                                        SEQUENCE OF 60-142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 17-26.
                                                                                          MEDLINE=89240739;
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SAP_BOVIN
                                                                                                                Query Match
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-!- FUNCTION: The lysosomal degradation of sphingolipids takes place by the sequential action of specific hydrolases. Some of these enzymes require specific low-molecular mass, non-enzymic proteins: the sphingolipids activator proteins (coprofeins).

-!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and galactosylceramide agalactosylceramide agalactosylceramide activates by combining with the enzyme and acidic lipid to form an activated complex, rather than by solubilizing
                                    Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P., Stevens R.L., Fubharty C.B., Fibharty A.L., "Structure of the asparagine-linked sugar chains of porcine kidney and human urine cerebroside sulfate activator protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-91285107; PubMed-2060627;
Schnabel D., Schroeder M., Sandhoff K.;
"Mutation in the sphingolipid activator protein 2 in a patient with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Saposin B stimulates the hydrolysis of galacto-cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1 agaqliosides by beta-galactosidase (EC 3.2.1.23) and globotriacosylceramide by alpha-galactosidase A (EC 3.2.1.22). Saposin B forms a solubilizing complex with the substrates of the
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                                                                                                                                                                                                                                                                                                                                        MEDLINE-99441404; PubMed=10510427;
Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,
Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,
"Carbinsty C.B., Fluharty A.L.;
"Cerebroside sulfate activator protein (Saposin B): chromatographic
and electrospray mass spectrometric properties.";
J. Mass Spectrom. 34:1040-1054(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90147748; PubMed=2302219; Menger D.A.; Zhang X.-L., Degala G., Wenger D.A.; Phong X.-L., Degala G., Wenger D.A.; Protection of a point mutation in sphingolipid activator protein-1 mRNA in patients with a variant form of metachromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,
O'Brien J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALFERNATIVE SPLICING.
MEDLINE=91210267; PubMed=2019586;
Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-55170731; PubMed-7866401; Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.; "Molecular genetics of metachromatic leukodystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sulfatide activator protein. Alternative splicing that generates three mRNAs and a newly found mutation responsible for a clinical
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Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 166:1017-1023(1990).
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                                                                                                                                                                                        J. Mass Spectrom. 35:1416-1424(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 266:7556-7560(1991).
MEDLINE=21110404; PubMed=11180632;
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FEBS Lett. 284:57-59(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sphingolipid hydrolases.
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A Morita N.;
"Saposin-C from bovine spleen; complete amino acid sequence and
relation between the structure and its biological activity.";
Elochim. Biophys. Acta 1120:75-80(1992).

I. Biochim. Biophys. Acta 120:75-80(1992).

E. PUNCTION: "HE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROPEINS:
THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROPEINS) (BY SIMILARITY).

C. !- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND
GALACTOSYLCERAMIDE BY BUTA-GALOGICERAMIDASE (EC 3.2.1.46).

SAPOSIN-C APPAREMILY ACTS BY COMBINING WITH THE ENYME AND ACIDIC
LIPPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SAPESIN B STIMULATES THE HYDROLYSIS OF GALACTO-CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GMJ GANGLIOGIDES BY BETA-CALACTOSIDASE (EC 3.2.1.23) AND GLOBOTRIADOSYLCERAMIDE BY APHA-GALACTOSIDASE A (EC 3.2.1.22). SAPOSIN B FORMS A SOLDHILIZING COMPLEX WITH THE SUBSTRATES OF THE SPHINGOLIPID HYDROLASES (BY SIMILARITY).

SPHINGOLIPID HYDROLASES (BY SIMILARITY).

SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).

SUBGINIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Lysosomal.
-!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence of the 
                                                                                                                                                                    Gaps
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-i- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                 ö
                                                                                              Length 524;
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Azuma N., Yoshida K.;
"RT-PCR cloning of bovine prosaposin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Score 40; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 AA.
                                                                                                                                                                 0; Mismatches
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MEDLINE=92207994; PubMed=1554743;
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                                                                                              60.6%;
62.5%;
                                                                                                                                                                    5; Conservative
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                                                                                                                                     Best Local Similarity
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01-AUG-1992 (Re
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                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-94272317; PubMed-8003952;
Sprecher-Levy H., Orr-Ortreger A., Lonal P., Horowitz M.;
"Murine prosaposin: expression in the reproductive system of a gene
        Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
MEDLINE=96084310; PubMed=8565332;
Calin W.R.;
"Expression of SGP-1 mRNA in preimplantation mouse embryos.";
Dev. Genet. 17:263-271(1995).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=Liver;
STADO Q.Q., Hay N.N., Morales C.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLUIAR LOCATION: Extracellular.
-! SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
-! SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tein; Repeat.

BY SIMILARITY.
SULFATED GIXCOROTEIN 1.
SAPOSIN-LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE A 2.
BY SIMILARITY.
                                                                                                    Tsuda M., Sakiyama T., Endo H., Kitagawa T.;
"The primary structure of mouse saposin.";
Biochem. Biophys. Res. Commun. 184:1266-1272(1992).
                                                                                                                                                                                                                                   implicated in human genetic disease."; Cell. Mol. Biol. 40:233-233(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97783; Psap.
InterPro; IPR003119; Sapa.
InterPro; IPR000046; Sapa.
InterPro; IPR0003159; Sapa.
InterPro; IPR000359; Saposin.
Pfam; PP02199; SAPA; 2.
ProDom; PD011232; SapB; 3.
ProDom; PD012321; Sap8; 3.
SWART; SW00162; SAPA; 2.
SWART; SW00118; SAPB; 4.
Sulfation; Signal; Glycoprotein; Re
                                                                     TISSUE=Liver;
MEDLINE=92272718; PubMed=1590788;
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                                                      SEQUENCE FROM N.A.
                      NCBI_TaxID=10090;
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          Mammalia;
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        the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SAPOSIN-LIKE TYPE B 1.
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SAPOSIN-LIKE TYPE B 4.
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   and the
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-> S (IN REF. 1).
293AFC0FB9C4FA99 CRC64;
 the Swiss Institute of Bioinformatics
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                                                                                                       EMBL; AB036791; BAA95677.1; --
PIR; S21770; S21770.
InterPro; IPR003119; SapA.
InterPro; IPR000004; SapB.
InterPro; IPR003299; Saposin.
Pfam; PF02199; SAPA; 2.
ProDom; PD001732; SapB; 3.
ProDom; PD012321; SapOsin; 1.
SMART; SM00162; SAPA; 2.
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Mus musculus (Mouse).
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525 AA;
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Matches 5; Conserv
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STRAIN=IMI 206040;
MEDLINE=95291429; PubMed=7773384;
Wasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma harzianum genes induced during growth on Rhizoctonia
                                         (POTENTIAL).
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Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBL_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology 141:767-774(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- INDUCTION: DURING MYCOPARASITISM.
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; Length 557;
Pred. No. 35;
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I -> V (IN REF. 2).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR002027; Amino_acid_permease.
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Pfam; PF00324; aa_permeases; 1.
PROSITE; PS00218; AMINO_ACID_ERMEASE_1; 1.
Transport; Amino-acid transport; Transmembrane.
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O9jhy3 mus musculu O9k911 bacillus ha O31623 bacillus su

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Minimum DB Maximum DB

Database

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STRAIN=FLORIO;
MEDLINE-20331236; PubMed=10891382;
Attout H., Billoir F., Biagini P., Cantaloube J.F., de Chesse R.,
De Micco P., de Lamballerie X.;
Sequence Determination and Analysis of the Full-Length Genome of
Colorado Tick Fever Virus, the Type Species of Genus Coltivirus
(Family Reoviridae).";
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EMBL; AF139759; AAG00068.1; -.
SEQUENCE 1182 AA; 135011 MW; EIF5F3515E9204C9 CRC64;
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Viruses; dsRNA viruses; Reoviridae; Coltivirus.
NCBL_TaxID=46839;
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Q94d19 homo sapien
Q9675 homo sapien
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Q1622 caenorhabdi
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Q1632 bepatitis g
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Q94894 thermotoga
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Q9C9X6
Q9LDE2
Q9SKD0
Q9UD19
Q9D929
Q99675
Q99675
Q968X2
P97587
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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016326
Q96898
041892
Q9WYF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL_19:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_mhc:*
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                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
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   STRAIN-CV. COLUMBIA;

XA MEDINE-21016719; Pubbwed-11130712;

XA Theologis A., Ecker J.R., Palm C.J.; Federspiel N.A.; Kaul S.,

XA Theologis A., Ecker J.R., Palm C.J.; Federspiel N.A.; Kaul S.,

XA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

XA White O., Alonso J., Chan H., Cheuk R.F., Chin C.W.,

XA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Lung M.K., Conn L., Chan T.V.; Feng J.-D.; Fong B., Fulji C.Y.,

A Lung J. L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

XA Langin-Hooper S., Lee A., Lee J. W., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

XA Langin-Hooper S., Lee A., Lee J.W., Henz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

XA Ead G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley B.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

XA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

XA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

XA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

XA Sageuence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R., Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.5; DB 10; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eaker J.R.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:816-820(2000).
EMBL, AC012563; AAG52002.1; -.
Hypothetical protein.
SEQUENCE 269 AA; 30392 MW; 2753AB3AD6063FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F10B6.5 (TSE21..17) (ATIG14680/F10B6.22).
Arabidopsis thaliana (Mouse-ear cress).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 16;
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                               HYPOTHETICAL 30.4 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Nuumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamannara Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                         Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Tambunga G., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT2G01930 PROTEIN.
AT2G01930.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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STRAIN-CV. COLUMBIA;
MEDLINE-20083487; Pubmed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.5; DB 10; Length 279;
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                                to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL, AC006917; AAF 9219.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AC010657; AAF63172.1; -.
EMBL, AY058073; AAL24181.1; -.
SEQUENCE 279 AA; 31168 MW; BAB996037E04D372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.;
"Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Ecker J.R.;
Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7; Conserva
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NCBI_TaxID=3702;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID≠10090;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                 Hayashizaki Y.;
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01-DEC-2001
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SEQUENCE
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   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carreasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-93003385; Pubmed-1390929; Kobayashi T., Makita A.; Kobayashi T., Honke K., Jin T., Gasa S., Miyazaki T., Makita A.; "Components and proteolytic processing sites of arylsulfatase B from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                Length 283;
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                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006532; AAF18588.1; -.
SEQUENCE 283 AA; 31648 MW; BAFBFCBD92262E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B003FB1459CA8FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                               Score 45.5; DB 10;
Pred. No. 17;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                64 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1159:243-247(1992).
                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-CCT-2000 (TrEMBLrel. 15, Last annotation
ARYLSULFAFASE B (EC 3.1.6.1) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
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                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                               68.98;
77.88;
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7270 MW;
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85.78;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TREMBLrel. 17,
1810009917RIK PROTEIN.
                                                                         Nature 402:761-768(1999).
                                                                                                                                                                                                    7; Conservative
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                                                                                   [2]
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                          (Human)
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P15848; 1FSU.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                           204 CYRWGCGGW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                     human placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AA;
                                                                                                                                                                                                                        1 cy-wgcgyw 8
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SEQUENCE
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Q9D929
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kinyoswa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsudo H., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Bronstein M.J., Bolluga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bolluga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Mashiwa-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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SEQUENCE FROM N.A.
Appel S., Bergheim A., Reichwald K., Reis A., Rosenthal A., Ramsay M.,
Hennies H.;
Hennies H.;
Hennies H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; ARO07402: BAB25015.1; -.
MGD; MGI:1916368; IB10009H17Rik.
SEQUENCE 212 AA; 24313 MW; 7D5EDF67496F61C4 CRC64;
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0
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Last annotation update)
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100.0%; Pred. No. 56;
iive 0; Mismatches
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42;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; Pubmed=11217851;
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100.0%; Pre
0; )
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RESULT 099675

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                                                                        Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                             STRAIN-ETSIER; TISSUE-FIBROBLAST;
MEDLINE=9712246; PubMed=8968090;
Madden S.L., Galella E.A., Riley D., Bertelsen A.H., Beaudry G.A.;
Miduction of cell growth regulatory genes by p53.";
Cancer Res. 56:5384-5390(1996).
EMBL: U66471; AAC52951.1; -.
InterPro: IPRO01841; Znf_ring.
SMART; SM00184; RING; I. Znf_ring.
SEQUENCE 332 AA; 37443 MW; D918EC9B74885104 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                 63.6%; Score 42; DB 11; Length 332;
100.0%; Pred. No. 64;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.6%; Score 42; DB 5; Length 342; Best Local Similarity 100.0%; Pred. No. 66; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AFOLG432; ARB65382.1; -
InterPro; IPR003002; 7TM_chemorecept_1.
InterPro; IPR000168; 7TM_nematode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
Geisel C., Wamsley P.;
"The sequence of C. elegans cosmid C07G3.";
submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6EF773489493954D CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 38.5 KDA PROTEIN.
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL GROWTH REGULATOR RCGR19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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342 AA; 38469 MW;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01461; 7tm_4; 1. Hypothetical protein. SEQUENCE 342 AA: 30157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                          Rattus norvegicus (Rat).
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"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                NCBI_TaxID=10116;
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98 CYWGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 cywgc 5
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Madden S.L., Galella E.A., Riley D., Bertelsen A.H., Beaudry G.A.;
Madden S.L., Galella E.A., Riley D., Bertelsen A.H., Beaudry G.A.;
Induction of cell growth regulatory genes by p53.";
Cancer Res. 56:5384-5390(1995).
-i. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL, U66469; AAC50897.1; -.
InterPro. IPRO01841; Znf_ring.
Pfam; PF00097; zf-C3FC4; 1.
SMART: SM00184; RING; 1.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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64;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO15063; AAH15063.1; -.
SEQUENCE 332 AA; 38268 MW; OFECCCE1E87950FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA; 38241 MW; 2F1FC0D12B710C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CELL GROWTH REGULATORY WITH RING FINGER DOWAIN.
                                                                                           (TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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100.0%; Pred. No. 64;
iive 0; Mismatches
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01-MAY-1997 (TrEMBLrel. 03, Created)
                                                          PRT;
                                                                                                                                                    CELL GROWTH REGULATOR CGR19.
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Best Local Similarity 100.
Matches 5; Conservative
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                                                          PRELIMINARY;
                                                                                                                                                                       Homo sapiens (Human).
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Best Local Similarity
Matches 5; Conserv
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98 CYWGC 102
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01-MAY-1997 (
01-DEC-2001 (
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P97587
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RESULT Q96BX2

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MEDINE-95241511; Pubmed-7724574; Simons J.N., Pilot-Matias T.J., Leary T.P., Dawson G.J., Desai S.M., Schlauder G.G., Muerhoff A.S., Erker J.C., Buijk S.L., Chalmers M.L., Van Sant C.L., Mushahwar I.K.; "Identification of two flavivirus-like genomes in the GB hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis GB virus A.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
NCBL_TaxID=39112;
                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RESTOL N2;
Geisel C., Wamsley P.;
The sequence of C. elegans cosmid C07G3.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                    "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF016432, AAB65377.1;
InterPro; IPR003002; 7TM_chamorecept_1.
InterPro; IPR00168; 7TM_nematode.
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agent.";
Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405(1995).
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100.0%; Pred. No. 67;
iive 0; Mismatches (
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[1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
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HCV_NS3.
HCV_NS4a.
HCV_NS4b.
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InterPro; IPR002518;
InterPro; IPR004109;
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InterPro; IPR001490;
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Geisel C., Wamsley P.;
"The sequence of C. elegans cosmid C07G3.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016432; ABB65378.1;
InterPro; IPR003002; 7TM_chemorecept_1.
InterPro; IPR001063; 7TM_nematode.
InterPro; IPR00154; HTH_GntR.
InterPro; IPR001307; Rhodanese.
Pfam; PF01461; 7tm_4; 1.
PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
PROSITE; PS00080; RHODANESE_1; UNKNOWN_1.
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347 AA; 38948 MW; BOBCF0891EB6AF57 CRC64;
                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 38.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.4 KDA PROTEIN.
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100.0%; Pred. No. 67;
tive 0; Mismatches (
                                                                                                                                                          347 AA.
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                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                        PRELIMINARY;
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                                    97 CYWGC 101
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          1 cywgc 5
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SEQUENCE 34
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ID D2323
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MEDLINE=97126113; PubMed-8971037;
MEDLINE=97126113; PubMed-8971037;
Leary T.P., Desai S.M., Yamaguchi J., Chalmers M.L., Schlauder G.G., Dawson G.J., Mushahwar I.K.;
"Species specific variants of GB virus A in captive monkeys.";
J. Virol. 70:9028-9030(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis GB Virus A.
Viruses; sRRNA positive-strand viruses, no DNA stage; Flaviviridae.
NCBI_TaxID=39112;
                      InterPro; IPR002166; HCV_RGRP.
InterPro; IPR002166; HCV_RGRP.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01006; HCV_NS54; 1.
Pfam; PF01001; HCV_RS54; 1.
Pfam; PF01001; HCV_RGRP; 1.
Pfam; PF01098; HCV_RGRP; 1.
PR05ITS: PS00011; PH0SPHOPANTETHEINE; UNKNOWN_1.
NONSITUCTURAL Drotein; POLYPROFIN; RNA-directed RNA polymerase.
SEQUENCE 2954 AA; 318833 MW; 4A0C35FCZED283B1 CRC64;
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MEDLINE-97437486; PubMed=9292019;
MEDLINE-97437486; PubMed=9292019;
Leary T.P., Desai S.M., Erker J.C., Mushahwar I.K.;
"The sequence and genomic organization of a GB virus A variant isolated from captive tamarins.";
J. Gen. Virol. 78:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 42; DB 12; Length 2954; 62.5%; Pred. No. 5e+02; 1ve 0; Mismatches 3; Indels (
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94421; AAB71133.1; -.
HSSP; P27958; 1HEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        041892 PRELIMINARY, PRT, 2967 AA.
041892;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN.
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InterPro; IPR002518; HCV_NS2.
InterPro; IPR004109; HCV_NS3.
InterPro; IPR000145; HCV_NS3.
InterPro; IPR000145; HCV_NS4a.
InterPro; IPR001868; HCV_NS5a.
InterPro; IPR002166; HCV_NS5a.
InterPro; IPR00166; Lipocla_cytFABP.
InterPro; IPR001005; Myb_DNA_bind.
Pfam; PF012907; HCV_NS2; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
InterPro; IPR002868; HCV_NS5a.
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
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Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Fluorine-18 (F-18) Fluorine-18 (F-18) Immunogenic peptid Human nerlyoeptide Human nerlyoeptide Human ORFX ORF2480 Human Cell growth Rat cell growth re A human cell growth Human sulfatase pr Human sulfatase pr Human sulfatase pr

Hepatitis GB virus Peptide #8830 enco Human brain expres Human bone marrow Peptide #9150 enco Human brain expres

AGG0113
AAG05113
AAG05612
AAY03716
AAY03716
AAY1629
ABB16263
AAY42908
AAA42908
AAA42908
AAA83424
AAA851184
AAG75458
AAB41334
AAA851133
AAA85113
ABB69676
AAA9966

Human polypeptide Drosophila melanog Muscarinic M3 rece Human protein sequ Novel human diagno Human activated T-FCTR4. Homo sapie

FCTR4. Homo sapie Somatostatin deriv Propionibacterium Arabidopsis thalia

AAB47327 AAY42915 AAU39355 AAG57261

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   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                Total number of hits satisfying chosen parameters:
                                                                         747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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A_Geneseq_032802:* | SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1985.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1990.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1991.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1991.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1991.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1992.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1995.DAT:* | SIDSI/gcgdata/hold-geneseqy-embl/AA1999.DAT:* | SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:* | SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:* | SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:* | SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Doc		Fluorine-18 (F-18)	Immunogenic peptid	Telomerase associa	H2 homologue of pr	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	
SUMMARIES	£		AAY03715	AAY76817	AAY66023	AAB18511	AAG40353	AAG60115	AAG05644	AAG38268	AAG40352	AAG60114	AAG05643
	ğ	;	20	21	21	21	21	21	21	21	21	21	21
	Length		æ	80	54	841	233	238	252	252	252	257	279
	& Query Match Length DR 1		100.0	100.0	72.7	71.2	68.8	68.8	68.9	68.8	68.8	68.8	68.8
	Score		99	99	48	47	45.5	45.5	45.5	45.5	45.5	45.5	45.5
	Result No.		1	7	m	4	5	9	7	æ	6	10	11

WO9911590-A1 11-MAR-1999.

X M X C

	ALIGNMENTS
# T11294	1 61
AAY	15
G X	AAV03715 standard; peptide; 8 AA.
AC	AAX03715;
×	
L	08-JUN-1999 (first entro)
XX	
DE	Fluorine-18 (F-18) labeled peptide 2.
XX	
ΚM	18F radionuclide; targeting vector; positron emission tomography; F-18;
ΚW	radiolabeling; thiol; fluorine-18.
XX	
os	Synthetic.
XX	
FΗ	Key Location/Oualifiers
FT	c-difference
FT	/note= "N-terminal acetylation; optionally has a free
FT	or protected thiol group"
FT	Misc-difference 2
FI	/note= "D-form residue"
FT	Misc-difference 3
FT	/note= "D-form residue"
ЕŢ	Misc-difference 5
FT	/note= "D-form residue; optionally has a free or
FT	protected thiol group"
FT	Misc-difference 7
FT	/note= "D-form residue"
FT	Misc-difference 8
FT	/note= "D-form residue"

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/note=
                        /note=
                                                                            'note=
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Best Local Similarity
                                                               Misc-difference 7
            Misc-difference 5
                                                                                       Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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Synthetic.
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                                                                                                                              W09966951-A2
                                                                                                                                                                                  22-JUN-1999;
                                                                                                                                                                                                            22-JUN-1998;
                                                                                                                                                                                                                       14-OCT-1998;
                                                                                                                                                        29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                              conjugates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                       into peptide-containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with cliuorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRRE2-(CH2)m-K, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising 1, Br. Cl. x azide, tosylate, mesylate, nosylate or triflate. n, m = 0-2; n+m = 0-2; x = 1, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, maleimide or optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl. R2 = I, Br. Cl. azide, tosylate, mesylate, triflate, H. COHH2, COOH, CH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl coptionally substituted by COHH2, COOH, OH, sulfonic acid, tertiary amine or quaternary ammonium, alkyl or phenyl. The method is used for Radiolabeling peptide-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "acetylated; modified with free amino acid group,
protected amino acid group, chelating agent or a
metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                            targeting vectors such as proteins, antibodies, antibody fragments and receptor targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences ARY03714-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                The invention relates to a method for incorporating 18F radionuclide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                             Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 66; DB 20;
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue" Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY76817 standard; peptide; 8 AA.
                                                                                                                                                                    Claim 14; Page 15; 22pp; English.
             98WO-US18268.
                                      97US-0057485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                               (IMMU-) IMMUNOMEDICS INC
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cywgcgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cywgcgyw 8
            03-SEP-1998;
                                     03-SEP-1997;
                                                                                         Griffiths GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY76817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY76817
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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprising administring a bi-specifically antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted lesson and at least 1 arm (B) that specifically binds a targeted lesson and at least 1 arm (B) that specifically binds in proteins are useful for pre-targetling methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                    "D-form residue; modified with free amino acid
group, protected amino acid group, chelating
agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McBride WJ,
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ilarity 100.0%; Pred. No. 6.4e+05;
Conservative 0; Mismatches 0;
"D-form residue"
                                                                                                                                                                                                                                  "D-form residue"
                                                                                                                                                                                                                                                                                                               /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 61; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US13879
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98US-0104156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hansen HJ, Griffiths GL,
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The present sequence represents a H2 homologue of a prolyl tripetididase (designated DPP) from Porphyromonas gingivalis. The prolyl tripeptidyl-peptidase has an amidolythic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the This bond is between a proline and an amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodonal disease such as gingivitis and periodontitis caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                              Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 21; Length 84
Pred. No. 1.5e+02;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thallana protein fragment SEQ ID NO: 50058.
                                                                                                                                                  (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                              Banbula A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Fig 6; 58pp; English
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990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
                                                                                                         99US-0123148
                                                             03-MAR-2000; 2000WO-US05551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                           Travis J, Potempa J,
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                                                                                                                                                                                                                                                                                                       WPI; 2000-594181/56.
                                                                                                                                                                       TRAVIS J.
POTEMPA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                    BANB/) BANBULA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 841 AA;
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                                                                                                       05-MAR-1999;
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25-MAR-1999;
29-MAR-1999;
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                    08-SEP-2000
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09-MAR-1999;
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                                                                                                                                                                       (TRAV/)
(POTE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence encoded by the gene;

(iii) comprise 0-10 amino acid from the carboxyl terminus of the normal part of the protein sequence preceding the amino terminus of the mutant sequence preceding the amino terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant in their full lengths or after processing by an antigen presenting cell (APC), T cell response.

The genes that the peptides are derived from, are characterised as antigen presenting cell (APC), T cell response.

The genes that the peptides are derived from, are characterised as susceptible to frameshiff mutation by having a mono nucleoside base repeat sequence of at least 5 residues, or a di-nucleoside base residues requence of at least 4 di-nucleoside base units. The peptides are created by the addition or deletion of 1 or 2 nucleoside base residues from the repeat sequence. The novel peptides and litit T cell responses and toxicity against tumours and cancer cells carrying genes with frameshift mutations. The novel peptides and DNA sequences can be used correct from the preparation of a composition for the treatment or prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAV55684-Y66142 are fragments of mutant proteins arising from a frameshift mutation in a gene from a cancer cell. The peptides are characterised in that they:

(i) are at least 8 amino acids long and a fragment of a mutant protein arising from a frameshift mutation in a gene of a cancer cell; (ii) consist of at least one amino acid of the mutant part of a protein (ii) consist of at least one amino acid of the mutant part of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
gingivitis; periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                     New peptides derived from genes with frameshift mutations, used to develop products for the treatment and prophylaxis of cancers
                                                                                                                                                                                                                                    Saeterdal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                  Moller M, Gjertsen MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H2 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 11;
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                                                                                                  99WO-NO00143.
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990S - 0.134219

990S - 0.134256

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     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 80;
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990S - 0159293 .
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990S - 0159329 .
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llarity 77.8%;
Conservative
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154 cyrwgcggw 162
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Pred. No. 82;
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173 cyrwgcggw 181
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16-MAY-1999;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 2123.
                                     AAG05643 standard; Protein; 279 AA.
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178 cyrwgcggw 186
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      99US-0148319.
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Best Local Similarity 77.00.
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Score 45.5;
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Gaps

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21; DB

Mismatches

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     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 93
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	7 00	12-OCE-1999;	2679CTO-5066	•					
	T A	13-0CT-1999;	9903 0158303 9911S-0159293	•					
	PR	13-0CT-1999;	99US-0159294						
	PR	13-OCT-1999;	99US-0159295						
_	PR	14-0CT-1999;	99US-0159329						
	PR	14-OCT-1999;	99US-0159330						
	PR	14-OCT-1999;	99US-0159331						
	PR	14-0CT-1999;	99US-0159637						
	PR	14-OCT-1999;	9908-0159638						
	PR	18-OCT-1999;	99US-0159584						
	7 G	21-OCT-1999;	99US-016U/41	•					
_	7 T	21-OCT-1999;	990S-0160/6/						
	PR	21-0CT-1999;	990S-0160770						
	PR	21-OCT-1999;	99US-0160814						
	PR	21-OCT-1999;	99US-0160815	ī					
	PR	22-OCT-1999;	99US-0160980	•					
	PR	22-OCT-1999;	99US-0160981						
	PR	22-OCT-1999;	99US-0160989	·					
	PR	25-OCT-1999;	99US-0161404						
	PR	25-OCT-1999;	99US-0161405						
	PR	25-OCT-1999;	99US-0161406	•					
	PR	26-OCT-1999;	99US-0161359	·					
-	PR	26-OCT-1999;	99US-0161360						
	PR	26-OCT-1999;	99US-0161361	•					
	PR	28-OCT-1999;	99US-0161920						
	PR	28-OCT-1999;	99US-0161992						
	PR	28-OCT-1999;	99US-0161993						
	PR	29-OCT-1999;	99US-0162142						
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	щ	cal Simi	arity 77.8%;	Pre		,		•	
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_	מבנ	search completed: August 17,		Z00Z, 1/:Z1:4Z					

Search completed: August 12, 2002, 17:21 Job time: 199 sec

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9.123 Million cell updates/sec
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Sequence 191, App
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-445-212-13
US-08-445-212-13
US-08-100-247-2
US-08-100-247-2
US-08-483-146A-2
US-08-484-126-1
US-08-753-829A-9
US-08-759-628-4
US-08-761-2488-12
US-08-602-999A-57
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US-08-415-751-6
US-08-905-223-452
US-08-901-435-2
US-08-931-047-2
US-08-796-899-28
US-08-943-956A-2
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-09-258-754-191
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                                                                                                                                                                                                                                                                                                                               231628 segs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                               August 12, 2002, 17:22:10
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Gapop 10.0 , Gapext 0.5
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Sequence:
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28 34 51.5 13 4 US-09-042-107-112 Sequence 112, App 29 34 51.5 13 4 US-09-042-107191 Sequence 191, App 30 34 51.5 13 2 US-08-761-248B-7 Sequence 7, Appli 32 34 51.5 212 2 US-08-761-248B-6 Sequence 6, Appli 33 34 51.5 220 2 US-08-761-248B-6 Sequence 6, Appli 34 51.5 220 2 US-08-761-248B-6 Sequence 7, Appli 34 51.5 220 2 US-08-761-248B-6 Sequence 7, Appli 35 34 51.5 292 3 US-08-811-90-3 Sequence 12, Appli 36 34 51.5 333 5 PCT-US93-08528-12 Sequence 12, Appli 37 34 51.5 376 1 US-08-608-241-2 Sequence 2, Appli 39 34 51.5 376 2 US-08-919-953-2 Sequence 2, Appli 40 34 51.5 376 4 US-09-192-983-2 Sequence 2, Appli 41 34 51.5 401 2 US-08-912-912 Sequence 2, Appli 42 34 51.5 401 2 US-08-912-911 Sequence 2, Appli 43 51.5 401 2 US-08-912-911 Sequence 10, Appli 44 34 51.5 726 4 US-09-312-10 Sequence 10, Appli 44 34 51.5 726 4 US-09-511-477-10 Sequence 10, Appli 45 31.5 726 4 US-09-511-10 Sequence 10, Appli 45 31.5 726 4 US-09-511-339 Sequence 339, Appli 45 339, Appli 45 34 51.5 726 4 US-09-511-339
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ALIGNMENTS

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RESULT 1

US-08-445-586-10

US-08-445-586-10

US-08-445-586-10

Sequence 10, Application US/08445586

Patent No. 520-5050

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Takeshita, Sunao

APPLICANT: Takeshita, Sunao

APPLICANT: Takeshita, Sunao

APPLICANT: Amann, Egon

TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and

TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and

TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and

TITLE OF INVENTION: Brocks:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

STREET: 1300 Inserte, N.W.

CONTRESPONDER EADABLES:

ADDRESSEE: Duncar Compatible

COMPUTER READABLE FORM:

CONTRY: USA

ZIP: ZONG-3314

CONTRY: USA

ZIP: ZONG-3314

CONGUTER: INM PC-COMPATA:

MEDIUM TYEE: Floppy disk

COMPUTER: INM PC-COMPATA:

APPLICANTON NUMBER: US/08/445,586

FILING DATE: 28-AUG-1992

PROOR APPLICANTON NUMBER: UP 230030/92

FILING DATE: 28-AUG-1992

PROOR APPLICANTON NUMBER: US-28-AUG-1992

PROOR APPLICANTON NUMBER: US-28-AUG-1992

PROTENTION NUMBER: 33,694

RESTSTREET: 20-2-408-400

TELEBEDATION NUMBER: 33,694

RESTSTREET: 20-2-408-400

TELEBEDATION OF SED ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: $33 amino acid

TOPOLOGY: INFORMATION acid
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Gaps
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Pred. No. 72;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                     APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhhodoro, Teresa
APPLICANT: Biolicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SOUTHWES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13, Application US/08345212; Patent No. 5932211; GENERAL INFORMATION:
                                 Sequence 13, Application US/08484494; Patent No. 5798239; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416;
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 516-742-4343
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Occhiodoro, Teresa
Bielicki, Julie
Clements, Peter R
Hopwood, John J
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEGUIENCE CHARACTERISTICS:
LENGTH: 533 amino acids
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Morris, Charles
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Best Local Similarity 85.7-
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-345-212-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
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63.6%; Score 42; DB 1; Length 533;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compartible
COMPUTER: TEM PC Compartible
COMPUTER: PER PC COMPACH
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PROOR APPLICATION: A24
PROOR APPLICATION: DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 31,346
REFERENCE/POCKET NUMBER: 84162
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                         APPLICANT: MITIS, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhhodoro, Teresa
APPLICANT: Dielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York CUTY: USA
                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                             Sequence 13, Application US/08484493
Patent No. 5728381
                                                                                           ;
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
                                                       63.6%;
85.7%;
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                   Ouery Match
Best Local Similarity 85./~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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US-08-445-586-10
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US-08-484-493-13
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Pred. No. 72;
0; Mismatches 1; Indels
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APPLICANT: O'BRIEN, JOHN S.

APPLICANT: O'BRIEN, JOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

ZIP: 9266

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,247

FILING DATE: 19930730

CLASSIFICATION: SIA
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: OBRIEN.002A
TELEPHONE: 619-235-8550

TELEPHONE: 619-235-9176

INFORMATION FOR SEQ ID NO: 2:
crotteneyer CLARRACTERISTICS:
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,003
                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,973
FILING DATE: 17-DEC-1992
ATTONNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE COOKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEFAX: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08100247 Patent No. 5571787
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-249-003-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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US-08-100-247-2
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Pred. No. 72;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09249003
| Patent No. 6153188
| GENERAL INFORMATION:
| APPLICANT: Wilson, Peter J
| APPLICANT: Morris, Charles P
| APPLICANT: Anson, Donald S
| APPLICANT: Occhiodoro, Teresa
| APPLICANT: Clements, Peter R
| APPLICANT: Clements, Peter R
| APPLICANT: Clements, Peter R
| APPLICANT: Hopwood, John J
| TITLE OF INVENTION: IDDRONATE 2-SULFATASE
| NUMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS:
          GLYCOSYLATION VARIANTS OF IDURONATE 2-SULFATASE 15
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF TITLE OF INVENTION: IDURONATE 2-SULFATASE NUMBER OF SEQUENCES: 15
ADDRESSEE: Scully, Scott, Murphy & Presser STREET 400 Garden City Plaza SITE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Scully, Scott, Murphy & Presser STREF: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:

CLASSIFICATION: 435
PILOR APPLICATION DATA:
APPLICATION NUBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                        ZIP: 11530
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%;
illarity 85.7%;
Conservative
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-345-212-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Matches 6; Conserv
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ZIP: 11530
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Dp ð

amino acid

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Sequence 2, Application US/08484594A
Fatent No. 5714459
GENERAL INFORMATION
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
TITLE OF INVENTION: DERIVED THEREFROM
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                              Sequence 3, Application US/08232513A
Patent No. 5700909
CENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 523;
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Pred. No. 1.38+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3
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FILING DATE: 21-APR-1994
CLASSIFFICATION DATA:
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: CAMPDELI, CARITYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.6%;
62.5%;
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amino acid
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Best Local Similarity 62.5°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                 San Diego
: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 CIWGPSYW 501
                                      494 CIWGPSYW 501
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1 cywgcgyw 8
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                                                                                                  RESULT 8
US-08-232-513A-3
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                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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Patent No. 5696080
GENERAL INFORMATION:
APPLICANT: O'BILEN, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
NUMBER OF SEQUENCES: 11
CORRESPONDENCE: 11
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                          Score 40; DB 1; Length 523
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FAST-SEQ for Windows Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/483,146A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Blvd. 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYELOS.002DV1
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NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                          60.6%;
62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: > 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                            HATI-SENSE: NO
FRAGHENT TYPE: N-terminal
FRAGHENT SOURCE:
CLONE: PROSAPOSIN
US-08-100-247-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                          Query Match 60.6
Best Local Similarity 62.5
Matches 5; Conservative
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                   TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                 494 CIWGPSYW 501
                                                                                                                                                                                                                                                                                                           1 cywgcgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
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Gaps ;

Length 30 3; Indels

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APPLICANT: Anderson, W. French
APPLICANT: Baltrucki, Leon F.
ASSELVENT AND TARGET B.
ADDRESSE: Carella, Stewart & Olstein
STREET: C. Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 62.5%; Pred. No. 17; 5; Conservative 0; Mismatches 3
     NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-134
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-520-2200
TELEPHONE: 919-530-2200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/326,347
FILING DATE: 20-COT-1994
APPLICATION NUMBER: 08/326,347
FILING DATE: 20-COT-1994
APPLICATION NUMBER: 08/326,347
FILING DATE: 09-NOV-1992
ATTORNEY AGENTE: 1FFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Ecotropic gp70 Protein
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Patent No. 5985655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                       ; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-753-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,778
REGISTRATION NUMBER: 31,778
REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 469 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6 becard CITY: Roseland STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cywgcgyw 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-126-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Juliano, Rudolph L.
APPLICANT: Juliano, Rudolph L.
APPLICANT: Juliano, Rudolph L.
APPLICANT: Juliano, Rudolph L.
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF
TITLE OF INVENTION: PEPTIDES THAT RECOGNIZE SPECIFIC DNA SEQUENCES
NUMBER OF SEQUENCES:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: 1211 East Morehead Street
CITY: Charlotte
STATE: No. 5869250th Carolina
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,829A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1; Les
Pred. No. 1.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                              OCHILLA SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,594A
FILING DATE: 07-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned &
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08753829A Patent No. 5869250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.6%;
62.5%;
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-484-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 CIWGPSYW 501
                                                                                                         USA
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US-08-753-829A-9
                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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Sequence 13, Application US/08895474

Sequence 13, Application US/08895474

Sequence 13, Application US/08895474

SEMENTAL INFORMATION:

APPLICANT: Nicola M.

APPLICANT: Gearing, David P.

APPLICANT: Gearing, David P.

APPLICANT: Metcalf, Donald

APPLICANT: Metcalf, David P.

TITLE OF INVENTION: Improvements in Granulocyte-Macrophage

TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: STENEY, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                   UROGENITAL SINUS DERIVED GROWTH FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 44; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 New York Ave., NW, Ste. 600
                                                                                                                                                                              COUNTRY: USA

ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILLING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
TELECHIONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35,723
ER: 34012.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICANT: ROWLEY,, DAVID R. TITLE OF INVENTION: UROGENIT TITLE OF INVENTION: FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.58;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 54.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: ||||
27 CFDGCGY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 cywgcgy 7
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US-08-895-474-13
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Rastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMALIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                           Score 38.5; DB 2; Length 469;
Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 4; Length 440 Pred. No. 2.9e+02; i. Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628 FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DX05520
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08759628 Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                               58.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                             Query Match 58.3
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-759-628-4
                                                                                                                                                                                      174 YWGCETTGRAYW 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                              2 ywgc----gyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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; Sequence 12, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
    US-08-484-126-1
                                                                                                                                                                                                                                                    RESULT 12
US-08-759-628-4
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DB 4; Length 31; ; s 0; Indels

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Score 35.5; Dl
Pred. No. 52;
0; Mismatches
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Job time: 198 sec
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.8%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                            ; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLEGULE TYPE: peptide
US-08-602-999A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cy----wgcg 6
|| || || || || 3 CYREKDTWGCG 13
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Sequence 57, Application US/08602999A

Fatent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: THORN, Judith M.

APPLICANT: TOUILLIAM, Lawrence A.

APPLICANT: FOWLKES, Dana M.

APPLICANT: FOWLKES, DANA METHODS OF TITLE OF THE M.

APPLICANT: FOWLKES, DANA M.

APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLING DATE: 16-JUL-1997
FILING DATE: 16-JUL-1997
CLASSIFRICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 1256.0030003
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2560
TELEPHONE: (202) 371-2560
SEDEMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITEET: ILDS AVENUE OI THE AMETICAS
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IEM PC COMPATIBLE
COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.8%; Score 35.5; D
Best Local Similarity 28.6%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CWWCCFFKWVQTRCKPDHGYW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cywgc----gyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-895-474-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-602-999A-57
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Mon Aug 12 17:16:15 2002

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 17:13:22; Search time 24.99 Seconds (without alignments)
30.761 Million cell updates/sec
Ferfect score: 59
Sequence: 19ywgkgyw 8
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 603
Minimum DB seq length: 8
Maximum DB seq length: 8
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*

Database :

	Description	epti		T-cell receptor be	T-cell receptor be	T-cell receptor ga	receptor	locustakinin - mig	ţ	triacylglycerol li	tubulin beta-3 cha	T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell receptor be	peptidylglycine mo	major fat-globule	pev-kinin 1 - pena	hypothetical pepti	0	leucokinin V - Mad	leucokinin VI - Ma	leucokinin VII - M	leucokinin VIII -	T-cell receptor be	T-cell receptor be	dissimilatory sulf	globulin IV alpha	Ig heavy chain CRD	T-cell receptor be
SUMMARIES	ID	JH02	E33932		PT072									PT0722				PD0029									S6349			PT0608
	DB	~	7	N	~	N	7	~	~	N	~	N	7	~	7	~	7	7	4	7	7	7	7	7	~	7	~	ď	7	7
	Length	2	7	9	7	9	4	9	9	7	7	7	7	7	7	7	7	7	7	8	æ	æ	œ	8	8	9	8	4	S	5
	Query Match	α.	/	3.9	9.6	2.5	8.8	28.8	8.8	8.8	89	8.8	8.8	8.	8.8	8.8	8.8	8.8	8.8	8.8	8.8	œ	æ	8	æ	5.4	S	æ.	3.7	e.
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	Score	25	22	20	20	19	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	15	15	14	14	14
	Result No.	7	7	Э	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	29

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Query Match 37.3%; Score 22; DB 2; Length 7; Best Local Similarity 60.0%; Pred. No. 2.8e+05; Matches 3; Conservative 2; Mismatches 0; Indels

2 ywgkg 6 ::||| 3 FYGKG 7

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14 23.7 6 2 151434 Earbellar degener 11 14 23.7 6 2 2521230 Cerebellar degener 12 14 23.7 7 2 521230 Cerebellar degener 13 22.0 6 2 2 2 2 2 2 2 2 2	LIGNMENTS e eel) n 31-Mar-1992 #text_change 11-Apr-1995 Muneoka, Y.; Ando, M. 28-832, 1991	ure and innection of a pencapeptide isolated from the gurber: JH0253; MUD:92062113 10253 1: protein 1: protein 2: cus> 1: protein 2: peptide increased basal tone of the circular muscle of troular muscle of the gastro-intestinal junction. 12: cular muscle of the gastro-intestinal junction. 142:4%; Score 25; DB 2; Length 5; 11: milarity 60 0%: Pred No 2 8e+65.	LOCAL SHRINALLY OU.US; Fred. NO. hes 3; Conservative 1; Mismatch 1 gwyk 5 1: 1 GFWNK 5	Ty mu chair D Fegion (E.) - mouse C:Species: Mus musculus (house mouse) C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996 C:Accession: E33932 B:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S. Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger A;Reference number: A33932; MUID:89282823 A;Status: preliminary A;Molecule type: mRNA A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-7 - CARQ-A A;Cross-references: GB:M27106 C;Reywords: immunoglobulin
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1 140.253 gut pentaper C, Species: R C; Date: 31.N C; Accession R; Uesaka, T B; acchemination	A; Reference num A; Accession: Ji A; Molecule type A; Residues: 1- A; Experimental C; Comment: This , and of the ci , and of the ci , and si Hest foral si	datches 1 1 SULT 2 19932	C; Species: 09-NC; Species: 09-NC; Date: 09-NC; Accession R; Baccala, Froc. Natl. A; Tille: Tww. A; Reference A; Accession: A; Status: pi A; Molecule: 4; Accession: A; Cross-reff C; Keywords: C; Reywords:

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A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-ul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
R;Reeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
                                                                                                                                                                                                                                                                             Firenery, A.J.

J. Exp. Med. 174, 115-124, 1991

A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Feference number: PT0509; MUID:91277601

A; Accession: PT0629

A; Accession: PT0629

A; Molecule type: mRNA

A; Residues: 1-6 <FEE>

A; Accession: PT0528

A; Status: translation not shown

A; Molecule type: mRNA

A; Residues: 1-6 <FEE>

A; Residues: 1-6 <FEE>

A; Experimental source: adult thymus, strain BALB/c, clone 100-4AB

C; Keywords: T-cell receptor
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C;Date: 17-dul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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                                                                                                                                          T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
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A;Status: translation not shown
A;Molecule type: DNA
A;Essidues: 1-7 <FES
C;Keywords: T-cell receptor
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75.0%;
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illarity 75.0%;
Conservative 0
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Decides: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
R;Harindranath, N; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 26, 881-8884, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Accession: B53284
A;Reference number: A33284; MUID:91342695
A;Accession: B53384
A;Residues: 1-4 <AARN-A;Residues: 1-4 <AARN-A;Residues: CB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A;Cross references: GB:S60737; NID:9233916; PIDN:AAB19518.1; NCBIP:60738)
C;Keywords: T-cell receptor
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R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, A;Reference number: A61068; MUID:92262851
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
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C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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Score 19; DB 2; Length 6; pred. No. 2.8e+05; l; Mismatches 2; Indels
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llarity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0;
          32.2%;
50.0%;
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          Query Match 32.2
Best Local Similarity 50.0
Matches 3; Conservative
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Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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Mon Aug 12 17:16:15 2002

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T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Accession: Pr0628
R.Feeney, A.J.
R.Feeney, A.J.
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N region: A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N region: A.Fitle: Junctional sequences of fetal R.Feeney A.Fitle: Junctional sequences of fetal R.Feeney A.F. Reference number: Pr0509; MUID:91277601
A.Accession: Pr0628
A.Status: translation not shown
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-7 < FEE>
A.Experimental source: newborn thymus, strain BALB/c
C.Keywords: T-cell receptor
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C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Accession: PT0642
R.Feenery, A.J.
B.Exp. Med. 174, 115-124, 1991
A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A.Refearence number: PT0509; MUID: 91277601
A.Recission: PT0642
A.Status: translation not shown
A.Mocession: PT0642
A.Stesidues: 1-7 <FEE>
A.Residues: 1-7 <FEE
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J. Exp. Med. 114, 115-124, 1991
J. Hitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A; Reference number: PT0509; MUID:91277601
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C;Species: Wus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0722
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Best Local Similarity
Matches 2; Conserv
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Kaboury 7

triacylglycerol lipase (BC 3.1.1.3) - Psychrobacter immobilis (fragment)

C;Species: Psychrobacter immobilis

C;Species: Psychrobacter immobilis

C;Species: Psychrobacter immobilis

C;Species: S50-001-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995

C;Accession: S57274

R;Arpigny, J.L.; Feller, G.; Gerday, C.

Biochim. Biophys. Acta 1263, 103, 1995

A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the

A;Reference number: S57274; MUID:95359197

A;Accession: S57274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-7 <ARP>

A;Cross-references: EMBL:X67712

C;Keywords: carboxylic ester hydrolase
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(Species: Drosophila melanogaster

(Species: Drosophila melanogaster

(Species: Drosophila melanogaster

(Species: Drosophila melanogaster

(Spacession: 83367

(Shinz, U.; Wolk, A.; Renkawitz-Pohl, R.

Development 116, 543-554, 1992

A; Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila vis A; Accession: 833567; MUID: 93170162

A; Status: preliminary; translation not shown

A; Molecule type: DNA
C: Accession: PT0637
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A: Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A: Reference number: PT0509; MUID:91277601
A: Accession: PT0637
A: Accession: PT0637
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Residues: 1-6 <FEE>
A: Experimental source: newborn thymus, strain BALB/C
C: Keywords: T-cell receptor
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A; Cross-references: EMBL:X68393; NID:97669; PIDN:CAA48459.1; PID:94377448
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Pred. No. 2.8e+05;
1; Mismatches 2; Indels
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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A;Cross-references: FlyBase:FBgn0003888
A;Introns: 5/3
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100.0%; Pre
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Matches 2; Conservative
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Matches 2; Conservative
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peptidylglycine monooxygenase (EC 1.14.17.3) form 3 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 23-Jun-1993
C;Accession: A38671
R;Stoffers, D.A.; Ouafik, L.; Eipper, B.A.
J. Biol. Chem. 266, 1701-1707, 1991
A;Title: Characterization of novel mRNAs encoding enzymes involved in peptide alpha-amid A;Reference number: A38671; MUID: 91107670
A;Accession: A38671
A;Status: preliminary; not compared with conceptual translation
A;Accession: A38671
A;Asolecule type: mRNA
A;Asolecule type: mRNA
A;Residues: 1-7 <STO>
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trecal receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0586; PT0592
R; Feeney, A.J. 14, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601
A; Title: Junctional sequences of A; Actaus: translation not shown
A; Actaus: translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-7 creba
A; Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN) and 141-1CD)
C; Keywords: T-cell receptor
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                                                                                                                                       Query Match 28.8%; Score 17; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
A; Residues: 1-7 <FEE>
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor
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lactobacill
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MEDLINE-92262851; PubMed-1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
"Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
-; FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angictensin-converting enzyme inhibitor.
Thunnus albacares (Yellowfin tuna) (Wochhunnus macropterus).
Thunnus albacares (Yellowfin tuna) (Wochhunnus macropterus).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostcmi;
Actinopterygii: Neopterygii: Teleostei; Euteleostei: Neoteleostei:
Acanthomorpha: Acanthopterygii: Percomorpha: Perciformes; Scombroidei:
NCBI_TaxID=8236;
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Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta; Pteryyota: Neoptera: Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acridoidea; Locusta.
P38644
P81864
P82073
P82055
P81865
P81841
P35904
P82158
P82158
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P42158
P42158
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6 AA; 654 MW; 686365A5B9CDB000 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  6 AA.
                                                                                                                                                                                                                                               ALIGNMENTS
                               RE32_LITRU
ASP2_LACSN
AL17_CARMA
ALL5_CALVO
ACH1_ACHFU
OCP1_OCTPI
ALL7_CYDPO
MNP1_LEPDE
                                                                                                                                                                        AL16_CARMA
ALL9_CARMA
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ilarity 100.0%; Pr
Conservative 0;
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MOD_RES 6 6
SEQUENCE 6 AA; 654 MW:
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TUBULES.
TOR8; A61068.
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Best Local Similarity
Matches 2; Conserv
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01-NOV-1995 (
15-JUL-1998 (
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P41491;
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LOK1_LOCMI
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ID ACI_THUAL
AC P1862
DT 01-NO
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23.592 Million cell updates/sec
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                                                                                                                      August 12, 2002, 17:15:03; Search time 13.13 Seconds
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P08939
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P33564
                                   Compugen Ltd
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                  105224 seqs, 38719550 residues
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WWA1_ACHFU
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RPCH_PANBO
RS1_ERWCH
RS7_MYCIT
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LOK1_LEUMA
LCK2_LEUMA
LCK3_LEUMA
LCK3_LEUMA
LCK4_LEUMA
LCK5_LEUMA
LCK6_LEUMA
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LCK7_LEUMA
LCK8_LEUMA

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AKHG_GRYBI
AKH_LIBAU
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AKH_TABAT
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Maximum Match 1008
Listing first 45 summaries
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"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of
Holman G.M., Cook B.J., Nachman R.J.;
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LCK4_LEUMA
C 0211143
DT 01-MAX
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LCK3_LEUMA
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MEDILINE=88326322; PubMed=3415688;
MEDILINE=88326322; PubMed=3415688;
Mobian Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                     Holman G.M., Cook B.J., Nachman R.J.; Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of
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01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin II (L-II).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                     Leucokinin I (L-I).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
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8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                            Biochem. Biophys. Res. Commun. 155:332-337(1988).
PIR; A31570; A31570.
SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;
                                                        Res. Commun. 155:332-337(1988).
                                                                                                                  28.8%; Score 17; DB 1;
100.0%; Pred. No. 1e+05;
iive 0; Mismatches 0
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
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MOD_RES 8 8
SEQUENCE 8 AA; 893 MW;
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Best Local Similarity
Matches 2; Conserv
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nes 2; Conserv
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P21141;
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P21140;
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LCK2_LEUMA
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-i- FUNCTION: THIS CEPHALDOWOTROPIC EPPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINGUT).

-i- SIMILARITY: TO THE OTHER LEUCOKININS.
Holman G.M., Cook B.J., Nachman R.J.; Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin III (b-III),
Leucophaea maderae (Madeira cockroach).
Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Orthopteroidea; Dictyoptera; Blattarla;
NCBL_TaxID=6988;
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
101-MAY-1991 (Rel. 18, Last annotation update)
101-MAY-1991 (Rel. 18, Last annotation update)
101-MAY-1991 (Rel. 19, Last annotation update)
101-MAY-1991 (Rel. 19, Last annotation update)
101-MAY-1991 (Rel. 18, Last annotation update
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8 AA; 910 MW; DC6365B449C866DA CRC64;
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8 AA; 852 MW; DC6365A5B9C8676A CRC64;
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MOD_RES 8 8
SEQUENCE 8 AA; 852 MW;
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Best Local Similarity
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P19989;
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-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY: OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
PIR; JS0315; JS0315.
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                                                                                                                                                                                                                                                                                              STIMULATES CONTRACTILE
                                                                                                   Holman G.M., Cook B.J., Nachman R.J.;
"Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
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01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leucokinin V (L-V)
Leucokin V (L-V)
Leucokin
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Pred. No. 1e+05;
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8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
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8 AA; 784 MW; 736365A5B9C865B8 CRC64;
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100.0%; Pred. No. 1e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                             Comp. Biochem. Physiol. 84C:271-276(1986).
-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE ST
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-1- SIMILARITY: TO THE OTHER LEUCOKININS.
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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100.0%; Pred. No. 100.0%; 0; Mismatches
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Leucophaea maderae (Madeira cockroach)
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Holman G.M., Cook B.J., Nachman R.J.;
Isolation, primary structure and synthesis of leucokinins VII and
VIII: the final members of this new family of cephalomyotropic
Peptides isolated from head extracts of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:31-34(1997).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARIY: JO THE OTHER LEUCOKININS.
PIR, JS0317; JS0317.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterzyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VII (L-VII).
Leucokinin VII (L-VII).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; NCBL_TaxID=6988;
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DC6365A5B9CDC76A CRC64;
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MOD_RES 1 1 1 1 MOD_RES 8 8 8 SEQUENCE 8 AA; 935 MW;
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Eŭkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
NCBI_Tax1D=82600;
                                                                                                                                                                                                                                                                                                                                                                                                using preparative two-dimensional gel electrophoresis.", Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
                                                                                                                                                                                                                    Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
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                                                                                                                                               01-ocr-1994 (Rel. 30, Created)
01-ocr-1994 (Rel. 30, Last sequence update)
01-FB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
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922879CABB58640D CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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MOD_RES 8 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iwakoshi E., Hisada M., Minakata H.; "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor "." Peptides 21:623-630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                         TISSUE-Head,

W. COOK B.J., Nachman R.J.;

Indonand G.M., COOK B.J., Nachman R.J.;

Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.",

Comp. Biochem. Physiol. 88C:31-34(1987).

-I. FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINGUT).

-I. SIMILARITY: TO THE OTHER LEUCOKININS.

PIR; JS0318; JS0318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Cardioactive, has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less
                                                                                                        Leucophaea maderae (Madeira cockroach).
Leucophaea maderae (Madeira cockroach).
Leucophaea; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 1; Length 4;
Pred. No. 1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-SERINE (IN OCP-4).
6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8 AMIDATION.
8 AA; 902 MW; 736365AB59CAADD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   active than Ocp-3.

- SUBCELLULAR LOCATION: Secreted.
-- PTM: Ocp-4 has D-Ser instead of L-Ser.
-- MASS SPECTROMETRY: MW-395.2; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Octopus minor (Octopus).
                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
   8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AA.
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     PRT;
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NCBI_TaxID=89766;
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                              Leucokinin VIII (L-VIII)
                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
     STANDARD;
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Matches 2; Conserv
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                                                                                                                                                                        Blaberoidea; Bla
NCBI_TaxID=6988;
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LCK8_LEUMA
P19990;
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P58649;
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SEQUENCE,
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MOD_RES
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RESULT 11 OCP3_OCTMI

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Query Match 20.3%; Score 12; DB 1; Length 8;
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MEDLINE-88234141; PubMed=3375140;

MEDLINE-88234141; PubMed=3375140;

MEDLINE-88234141; PubMed=3375140;

MEDLINE-88234141; PubMed=3375140;

MEDLINE-88234141; PubMed=3375140;

MEDLINE-8823411; PubMed=3375140;

Marsupials.";

Marsupials.";

Marsupials.";

MARSUPIAL SPEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION

THE BRAIN IS NOT CLEAR.

MAD THE RELEASE OF PANCERATIC ENZYMES IN THE GUT. ITS FUNCTION

THE BRAIN IS NOT CLEAR.

C. -1- SIMILARIY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

PIR; PQ0012; PQ0012.

PROSITE; PS00129; GASTRIN; 1.

MANDARES 2

SULFATION.

THOS. PROSITE; PS00259; GASTRIN; 1.

MANDARES 2

SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liljeqvist J.-A., Svennerholm B., Bergstrom T.,
Submitted (APR-1999) to the SWISS-PROT data bank.
-!-MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSVI AND
2: GH, GB, GC, GG, GD, GI, AND GE.
-!-MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   CCK.

CCK.

Macropus eugenii (Tammar wallaby), and
Dasyuus viverrinus (Southeastern quoll).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCHL_TaxID=9315, 9279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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VGLG_HSV2B
STANDARD; PRT; 8 AA.

PGLG_HSV2B
STANDARD; PRT; 8 AA.

PGLT01999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
OC VILLS SIMPLES SIMPLES, NORMA STAGE; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OC Alphaherpesvirinae; Simplexvirus.
ON NCBL_TAXID-103921;
RN | 1|
RP SEQUENCE
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -! MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEIN
CC -: MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-CC HSV-I.
KW Glycoprotein.
RT NON.TER 8 AA; 683 MW; 7B47686772C865B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
DDCAA68378768B5A CRC64;
                                                                                                        P30369;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Cholecystokinin (CCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12; DB 1;
Pred. No. 1e+05;
                                                                                     8 AA.
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                                                                                     PRT;
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llarity 66.7%;
Conservative
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                                                                                 STANDARD;
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Best Local Similarity
Matches 2; Conserv
                                                                                 CCKN MACEU
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RESULT 14
CCKN_MACEU
ID CCKN_MACEU
DT 01-APR
DT 01-APR
DT 01-OCT
DE Cholec
GN CCK.
OS MACTOF
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Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: August 12, 2002, 17:20:43 Job time: 340 sec

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P82065 litoria rub

047029 P82065 009258 085406 044463 056429

enterobacte P82096 litoria

009258 synechococc 085406 coxtella bu 085402 thermus the 055429 thermus the 0938p2 pseudomonas 015890 homo saplen 094ry3 sus sp. ins 095792 saccharomyc 095792 saccharomyc 094ry3 varanus ind 094vef varanus ind 094vel varanus rud 094vbb varanus sal 094vb varanus sal 094vb varanus sal 094vb varanus sal

015890 09VRDZ 09VRDZ 095MZ3 095MZ3 0914VZ 094VE6 094VE6 094VB5 094VB5

varanus yuw felis silve felis libyc felis silve

094px7 094px6 094px5

ALIGNMENTS

varanus v varanus

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049223 glycine max P82685 periplaneta P82686 periplaneta P82689 periplaneta P82689 periplaneta P82689 periplaneta P82699 periplaneta P82699 postiplaneta Q956771 alfalfa mos Q95772 shiqella dy Q15889 homo sapien 002831 oryctolagus Q95513 oryctolagus Q95545 saccharomyc Q91071 rattus norv
                                                   August 12, 2002, 17:14:38; Search time 39.45 Seconds (without alignments) 35.081 Million cell updates/sec
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             Compugen Ltd.
                                                                                                                                                               Total number of hits satisfying chosen parameters:
    GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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P82685
P82686
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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Match Length
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ö Glycine max (Soybean).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847; SEQUENCE FROM N.A.
STRAIR=CV. ESSEX; TISSUE=ROOT;
MEDLINE=91367679; PubMed=1891369;
Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins."; Gaps .; 0 Length 7; Indels STRAIN=CV. ESSEX; TISSUE-ROOT;
Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF047050; AAC03556.1; -. 049223; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HMG-1-LIKE PROTEIN (FRAGMENT). 7 AA; 850 MW; 6AAAAAB378637810 CRC64; 28.8%; Score 17; DB 10; 1 llarity 100.0%; Pred. No. 5.6e+05; Conservative 0; Mismatches 0; Ą. Nucleic Acids Res. 19:4769-4769(1991). PRELIMINARY; Query Match Best Local Similarity Matches 2; Conserv SEQUENCE FROM N.A. SEQUENCE WG - WG 049223 Н ŏ q

002831 095213 095945 09UCN4 062721

064971 09R5R2 Q15888 ~

P82685; P82685

RESULT P82685

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TISSUE-CORPORA CARDIACA;
MEDLINE-98010462; PubMed-9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=CORPORA CARDIACA;
MEDLINE=98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGGIL PEPL. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.8%; Score 17; DB 5; Length 8; 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-4 (PEA-K-4).
                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-3 (PEA-K-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 8 AN AMIDATION.
8 AA; 909 MW; DC6365B449D5A76A CRC64;
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                                                                                                                                        8 AA.
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                                                                                                                                                                                                                                                           Periplaneta americana (American cockroach).
                                                                                                                                        PRT;
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MOD_RES 8 8
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                                                                                                                                          PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6978;
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SEQUENCE
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MEDLINE-98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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"Isolation and structural elucidation of eight Kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana.";
                                                                                                                                 Oliman 2007.

Reriplaneta americana (American cockroach).

Periplaneta americana (American cockroach).

Mataroda; Insecta;

Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria,
Blattoidea, Blattidae, Periplaneta.
                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                            REGUL. PEPT. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
NEULOPEPTIGE; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regul. Pept. 71:199-205(1997).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;
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8 AA; 950 MW; 326365B449D5A774 CRC64;
                                         8 AA.
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-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
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Periplaneta americana (American cockroach).
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MEDLINE=98010462; PubMed=9350979;
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MOD_RES 8 8
SEQUENCE 8 AA; 856 MW;
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Matches 2; Conservative
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U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
MATOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
Bukaryota, Hotzaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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TISSUB-CORPORA CARDIACA;
MEDLINE-98010462; Pubmed-9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-5 (PEA-K-5).
Friblaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Periplaneta mericana (American cockroach).
Butaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         americana.";
Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                        28.8%; Score 17; DB 5; Length 8; 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0; Indels
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8 AA; 865 MW; C76365B449CDC775 CRC64;
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SIMILARITY: BELONGS TO THE KININ FAMILY
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Query Match
Best Local Similarity 100...
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MOD_RES 8 8
SEQUENCE 8 AA; 865 MW;
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Matches 2; Conservative
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TISSUE=LIVER;
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                                                                                                                                                     Gaps
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Nucleic Acids Res. 8:5635-5647(1980).
BELL: V00047; CAA23416.1; -.
NON TER
SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;
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SEQUENCE FROM N.A.

Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
Bol J.F.;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Alfamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                   Length 8;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRUNCATED PROTOPORPHYRINOGEN OXIDASE (FRAGMENT).
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                        935 MW; 9639D1A72058637D CRC64;
                                                                                                28.8%; Score 17; DB 6; Le Lalarity 100.0%; Pred. No. 5.6e+05; Conservative 0; Mismatches 0;
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Mol. Genet. Metab. 73:91-96(2001).
Embl. AF32182; AAK69608.1; -.
NON TER
SEQUENCE 8 AA, 862 MW; 893365Bi
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8 AA;
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STRAIN=F-I/RGM;
Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
"Rabbit DQ52 and DH Gene Rearrangements in Early B-cell Development.";
MO1. Immunol. 0:0-0(1996).
EMBL; U62585; AAB18735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Vuorio E.;
"Evidence for insufficient chondrocytic differentiation during repair
of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last annotation update)
PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDINE=96377339; PubMed=8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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C1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
C1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GERMLINE DH (DF) GENE (FRAGMENT).
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8 AA; 1028 MW; B859C7272EA77371 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.0%;
Best Local Similarity 50.0%;
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SEQUENCE FROM N.A.
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SEQUENCE 8 AA; 902 MW; FE2DCAFB586AE336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y., Caskey C.T.H.;

Lastey C.T.H.;

Tisolation of chromosome-specific genes by reciprocal probing of arrayed cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL: L32069; AAA73878.1; -.

NON_TER B B

SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
31,000 DA PRODUCT OF ORFB.
Shigella dysenteriae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                    Length 8;
                                                           1; Indels
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                  25.4%; Score 15; DB 12;
66.7%; Pred. No. 5.6e+05;
tive 0; Mismatches 1;
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                                                                Conservative
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TISSUE-PLACENTA;
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8 AA;
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NCBI_TaxID=622;
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Q15888;
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Q15888
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BUDIAN=81069885; Pubmed-6254986;

BODIZ S.G., COTUZZI G., Thalenfeld B., Tzagoloff A., Macino G.;

"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytcchrone oxidase.";

J. Biol. Chem. 255:11941(1980).

EMBL; V00694; CAA24066.1; -...
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Mitochondrion.
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Sacc
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SEQUENCE 8 AA; 689 MW; 8088733DD33DD87D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE
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                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INSIDE INTRON 5 (FRAGMENT).
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50.0%;
                                                                    PRELIMINARY;
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Best Local Similarity 50.0
Matches 3; Conservative
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RESULT 14
Q95945
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Fluorine-18 (F-18)	Fluorine-18 (F-18)	Immunoaenic pentid	Fluorine-18 (F-18)	Immunogenia pentid	RGD conta pentide	Lvcium B peptide	Moraxella catarrha	Moraxe]]a catarrha	Core nolvnentide f	Viral DP178/107-11
SUMMARIES		ID	AAY03714	AAY03716	AAY76818	AAY03715	AAY76817	AAR57814	AAR11895	AAW46276	AAW46279	AAY89518	ABB00926
		DB	20	20	21	20	21	15	12	19	19	21	22
æ		Match Length DB	œ	80	80	80	ω	9	00	7	œ	œ	80
	Query	Match	100.0	100.0	86.4	76.3	76.3	55.9	50.8	47.5	47.5	47.5	47.5
		Score	59	59	51	45	45	33	30	28	28	28	28
	Result	No.	1	7	m	4	2	9	7	80	σ	10	11

11-MAR-1999.

Viral core polypep DP178-11ke/DP107-1 Core polypeptide T RGD contg. peptide RGD contg. peptide RGD contg. peptide	RGD contg. peptide G. oxydans cytochr Anti-b-endorphin m Beta-endorphin N-t Membrane dipeptida Antiproliferative	peptid peptid de corr ogenic o-endor	venom d venom d venom d venom d etic SCM etic SCM	Silk spider fibrol Dynorphin-like pol Snake venom derive T-cell receptor CD Snake venom derive Snake venom derive Snake venom derive Human ART-l peptid T-cell receptor co
22225	5 AAR57803 2 AAY97759 3 AAR20449 6 AAR70043 6 AAR48621 5 AAR60436	AAW2268 AAW2268 1 AAB2788 6 AAR7864 3 AAR7569 5 AAR4569	AAY1598 AAW5048 9 AAW5041 9 AAW5035 0 AAP9177 0 AAY3339	2 AAR61040 9 AAR61040 9 AAW57625 9 AAW57626 9 AAW50466 9 AAW50406 1 AAW50340 1 AAW503894 1 AAY88615
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12 13 14 15 16	18 19 20 22 23	22 22 24 24 25 24 25 25 26 26 26 26 26 26 26 26 26 26 26 26 26	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	, w w 4 4 4 4 4 , w 0 0 0 1 1 1 1 1 1 1 1 1

ALIGNMENTS

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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                        /note= "D-form residue; optionally has a free protected amino acid group"
                                                                                                                                                                    /note= "optionally has a free or protected amino acid group"
                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                   /note= "D-form residue"
                                                                                                                                                                                                                                                                       /note= "D-form residue"
                                                                                                                                                                                                                                                                                          /note= "D-form residue"
                                                                              Fluorine-18 (F-18) labeled peptide 1.
                                                                                                                                                   Location/Qualifiers
                    AAY03714 standard; peptide; 8 AA.
                                                           (first entry)
                                                                                                                                                                                       Misc-difference 2
                                                                                                                                                                                                                                                           Misc-difference 7
                                                                                                                                                                                                           Misc-difference 3
                                                                                                                                                                                                                                Misc-difference 5
                                                                                                                                                   Key
Misc-difference
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                             WO9911590-A1
                                                           08-JUN-1999
                                                                                                                               Synthetic.
                                       AAY03714;
             AAY03714
RESULT
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
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                                                                                                                                                                             03-SEP-1997;
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                                                                                     WO9911590-A1
                                                                                                                   11-MAR-1999
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         continuous peptide-containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with camission tomography. Radiolabeling thiol-containing peptides with calculations of F-18 comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-(CM2)m-CRIR2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                             radionuclide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                  Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                             The invention relates to a method for incorporating 18F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "D-form residue; D-iodo-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 20; 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-terminal acetylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY03716 standard; peptide; 8 AA.
                                                                                                                                                                                               Claim 13; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
               98WO-US18268
                                          97US-0057485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                          (IMMU-) IMMUNOMEDICS INC
                                                                                                                                    WPI; 1999-228967/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
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Modified-site
               03-SEP-1998;
                                            03-SEP-1997;
                                                                                                        Griffiths GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Matches
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Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
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0
/note= "D-form residue; optionally acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                     Radiolabeling thiol-containing peptides with fluorine-18
                            "D-form residue; D-iodo-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 59; DB 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0;
                                                       "D-form residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY76818 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                 Claim 15; Page 15; 22pp; English.
                                                                                                                                            98WO-US18268.
                                                                                                                                                                      97US-0057485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                   (IMMU-) IMMUNOMEDICS INC.
                             /note=
                                                          /note=
                                                                                                                                                                                                                                                        WPI; 1999-228967/19.
                                         Misc-difference 8
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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.

Location/Qualifiers

Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to complex, therapeutic agent or diagnostic agent can be varied to antibodies differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or expectable conjugate that is capable of carrying at least 1 diagnostic or expectable conjugate that is capable of carrying at least 1 diagnostic or expectable conjugate that is capable of carrying at least 1 diagnostic or expectable conjugate that is capable of carrying at least 1 diagnostic or expectable conjugate that the capable of carrying at least 1 diagnostic or expectable conjugate that the capable of carrying at least 1 diagnostic or expectable conjugate that the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable confusion and the capable of carrying at least 1 diagnostic or expectable 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Z;
                                                                                                                                                                                                                       'note= "acetylated D-form residue"
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Pred. No. 6.4e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McBride WJ,
                                                                                                                        "D-form iodo-Tyr"
                                                                                                                                                                                                                                                                      'note= "D-form iodo-Tyr"
                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                    /note= "D-form residue"
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                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leung S,
                                                                       /note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY03715 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0090142.
98US-0104156.
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ilarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMU-) IMMUNOMEDICS INC.
                                                                                                                           /note=
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Best Local Similarity
?; Conservē
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                                                                                            Misc-difference 2
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| gywhkgyw 8
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                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hansen HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conjugates
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ID AAY0
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qq
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into periodical restricts to a method 101 incorporating late radional position of the periodical restricts of a method 101 incorporating a periodic comprission and free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-X, or group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)m-X, or a fluorinated alkene in which at least one of the two double bonded a fluorinated alkene in which at least one of the two double bonded azide, tosylate, mesylate, nosylate, in = 0-2; n+m = 0-2; x = 1, Br, CI, azide, tosylate, mesylate, nosylate, triflate, maleimide of coptionally substituted by 12 alkyl) or 3-sulfomaleimide; R1, R2 = 1, Br, CI, azide, tosylate, mesylate, triflate, H, COMH2, COOH, CH, Sulfonic acid, tertiary amine, quaternary ammonium, alkyl (OH 20, COMR2) or quaternary ammonium, coor, or quaternary ammonium, coor, COMR2 or CORY; and R' = 1-6C alkyl or phenyl. The method is used for Radiolabeling peptide-containing targeting vectors such as proteins, antibodies, antibody fragments and receptor-targeted peptides for use in routine clinical positron the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0314-116 represent the samples of F-18 labeled peptides used in the method of detecting a samples of examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                 /note= "N-terminal acetylation; optionally has a free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                    /note= "D-form residue; optionally has a free or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                      or protected thiol group"
                                                                                                                                                                                                                                                         protected thiol
                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                       /note= "D-form residue"
                                                                                                                                                                    /note= "D-form residue"
                                                                                                                                                                                                                                                                                       /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.3%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US18268
                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0057485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-228967/19.
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Best Local Similarity
                                                                                   Key
Misc-difference
                                                                                                                                                 Misc-difference
                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ywgcgyw 8
                                                                                                                                                                                                                                                                                                                                                       WO9911590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths GL;
                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
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Length 8;

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AA;
                                                              2 ywgcgyw 8
                                           2 ywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          æ
                                                                                                                                                                                                                                                                                                                            07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                  07-SEP-1992;
18-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 wgrgdw
                                                                                                                                                                    03-OCT-1994
                                                                                                                                                                                                                                                                                  WO9405696-A.
                                                                                                                                                                                                                                                                                                       17-MAR-1994.
                     9
                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                            AAR57814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR11895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                  9
                    Matches
                                                                                                               AAR57814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR11895
                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable complex, therapeutic agent or diagnostic and be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The taristing new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                 /note= "acetylated; modified with free amino acid group,
protected amino acid group, chelating agent or a
metal-chelate complex"
                                                                                                                      Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                           "D-form residue; modified with free amino acid
                                                                                                                                                                                                                                                                                                      group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                  Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leung S, McBride WJ,
                                                                                                                                                                                                                                                                                                                                       /note= "D-form residue"
                                                                                                                                                                                                                                               /note= "D-form residue"
                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                             /note= "D-form residue"
                                                                                                                                                                              Location/Qualifiers
                              AAY76817 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 61; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0090142.
                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US13879
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-160561/14.
                                                                                                                                                                                                                                                                                                                            Misc-difference 7
                                                                                                                                                                                                                                     Misc-difference 2
                                                                                                                                                                                                                                                           Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1998;
                                                                           28-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conjugates
                                                                                                                                                         Synthetic
                                                     AAY76817;
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                  AAY76817
         RESULT
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptides given in AAR57801-28 have antithrombotic, anticoagulant
                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides and their salts - used in platelet prepns., as antithrombotic agents and as inhibitors of e.g. cell adhesion, cancer metastasis and extracorporeal circulation coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Platelet; antithrombotic; inhibitor; cell adhesion; cancer; metastasis; extracorporeal circulation; coagulation; anticoagulant; cell fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 15; Length 6;
Pred. No. 6.4e+05;
1; Mismatches 1; Indels
76.3%; Score 45; DB 21; Length 8; 85.7%; Pred. No. 6.4e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and cell fusion inhibiting effects. They may be used in
antithrombotic agents and as extracorporeal dirculation
coagulation inhibitors, cell adhesion inhibitors, cancer
metastasis inhibitors and protecting agent in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGD contg. peptide having antithrombotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 52; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR11895 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                                               AAR57814 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-JP01262.
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93JP-0203962.
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YAWA ) NIPPON STEEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-1991 (first entry)
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preparations. (IC50 = 2.2 \times 10 -5 M).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Katada J, Sato Y;
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This peptide corresponds to amino acid residues 296-302, in the non-conserved region 1, of the outer membrane protein CopB (see AMW4621) of Moraxella catarrhalis strain 035E. Claimed isolated peptides of about 5-60 amino acid residues comprise at least this 7-amino acid peptide sequence and are reactive with monoclonal antibody 10F3. The 7-amino peptide is most preferred for binding to 10F3. It is located C-terminal to the Asn-295 cesidue of CopB that influences the binding kinetics of the epitope. Peptides which contain residues C-terminal to Asn-295 retain reactivity, but this reactivity is less than that obtained in the presence of Asn-295. Claimed peptides (see AAW46274-84) from non-conserved region I can be used in the diagnosis, prophylaxis (as vaccines) and treatment of M. catarrhalis infections.
                                                                                                                                            New isolated Moraxella catarrhalis peptide(s) - which define epitopes of the outer membrane protein used to develop products for the diagnosis, prophylaxis and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Moraxella catarrhalis peptide(s) - which define epitopes of the outer membrane protein used to develop products for \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CopB; outer membrane protein; epitope; infection; diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 19; Length 7; Pred. No. 6.4e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis CopB region I epitope.
                                                                                                                                                                                                          Claim 3; Page 113; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis strain 035E.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46279 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.5%;
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             96US-0023832
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                                              (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                             WPI; 1998-159542/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                             Cope
            12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ywgkgy 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                               Aebi C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                     Lycium; angiotensin converting enzyme; renin; hypertension; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This lycium B peptide has angiotensin converting enzyme (ACE) and renin inhibiting activity and can be used in the treatment of hypertension. It is used in the form of a drug compsn. Residue 4 (Gl\gamma) is modified by calcium and residue 8 (Tr\rho) has an indol gp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane protein; epitope; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide(s) lyciumin A and B - have ACE and renin inhibiting activity for treatment of hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 12; Length b;
Pred. No. 6.4e+05;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis CopB region I epitope.
                                                                                                                                                                                                                     /note= "tryptophan indol"
                                                                                                                        /note= "pyroglutamyl"
                                                                        Location/Qualifiers
                                                                                                                                                                        /note= "glycyl Ca"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxella catarrhalis strain 035E.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; page 1; 6pp; Japanese.
                                                                                                /label= OTHER
                                                                                                                                                     /label= OTHER
                                                                                                                                                                                                     /label= OTHER
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                    (NIME-) NIPPON MEKTRON KK.
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les 4; Conservative
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      Lycium B peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CopB; outer membi
therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA;
                                                                                    Modified-site
                                                                                                                                     Modified-site
                                                                                                                                                                                    Modified-site
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3 wgvgsw 8
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                                                                                                                                                                                                                                                                                                                                                    23-AUG-1989;
                                                                                                                                                                                                                                                                                  05-APR-1991.
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Sequence

present.

Query Match

Matches

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AAW46276 RESULT

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Gaps

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                                                                                                                                                                                                                                                                                                 ABB00926;
                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                       Viridiae.
                                                                                                                                                                                                                                                              ABB00926
                                                                                                                                                                                                                                                                                                 pp
 2555555555<u>x</u>8
                                                                                                                                                                                            δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (9p41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bloactive peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-1ife; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
                                                                                                                                                                                                                                                    Gaps
                                                        non-conserved region 1, of the outer membrane protein CopB (see AAW46271) of Moraxella catarrhalis strain 035E. Claimed isolated peptides of about 5-60 amino acid residues comprise at least this 8-amino acid residues comprise at least monoclonal antibody 10F3. The 8-amino peptide is most preferred for binding to 10F3. It includes the Asn-295 residue of CopB that is required for 10F3 binding. Claimed peptides (see AAW46274-84) from non-conserved region 1 can be used in the diagnosis, prophylaxis (as vaccines) and treatment of M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence -
                                               This peptide corresponds to amino acid residues 295-302, in the
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                                                                                                                                                                                                                           Score 28; DB 19; Length 8;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
the diagnosis, prophylaxis and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anwer MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Core polypeptide fragment T No. 1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 39; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merutka G,
                        Claim 6; Page 113; 132pp; English
                                                                                                                                                                                                                                                                                                                                                            AAY89518 standard; peptide; 8 AA.
                                                                                                                                                                                                                              47.5%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                        Similarity
5; Conserva
                                                                                                                                                                                           8 AA;
                                                                                                                                                                                                                                                                         2 ywgkgy 7
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3 yagkgy 8
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                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-NOV-1999
                                                                                                                                                                    nfections
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Best Local S
Matches 5
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                                                                                                                                                                                            Sequence
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selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erickson JB, Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viral DP178/107-like region peptide T1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB00926 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
                                                                                                                                                                                                                    /note= "N-terminal is substituted by Ac"
                                                                                                                                                            Human immunodeficiency virus 1 isolate LAI.
                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                      DP178-like/DP107-like peptide T-1076.
                                                                                                                                                                                               Location/Qualifiers
                                     AAU13472 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                99US-0350841.
                                                                                                                                                                                                                                                                                                          05-JUL-2000; 2000WO-US35727
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                       (TRIM-) TRIMERIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442157/47
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                                                                                                                                                       Modified-site
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                                                                                 21-NOV-2001
                                                                                                                                                                                                                                                                                      19-JUL-2001.
                                                                                                                                                                          Synthetic
                                                           AAU13472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated analogues of the heptad repeat region peptides pp178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heptad repeat region peptide analogs useful for inhibiting virus/cells fluston, useful for treating HIV and Respiratory Syncytial Virus infection -
                                                                                                                                                                                                                                                                    Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
infection.
                                                                               Gaps
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                                                    Score 28; DB 22; Length 8;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambert DM,
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tches 1;
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                                                                                                                                                                                                                                               Viral core polypeptide, SEQ ID NO: 919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 410; 587pp; English.
                                                                                                                                                                           ABB02392 standard; Peptide; 8 AA.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                      29-FEB-2000; 2000US-0515965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antczak JB, Delmedico MK,
                                                                                                                                                                                                                        03-JAN-2002 (first entry)
                                                   Query Match 47.5
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             (TRIM-) TRIMERIS INC.
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the specification.
                      8 AA;
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                                                                                                                                                                                                                                                                                                                                      WO200164013-A2
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                     Sequence
                                                                                                                                                                                                   ABB02392;
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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise activity. The peptides of the invention (AAU12559-AAU14009) comprise DB178-like and DB107-like peptides. The DB178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus I (HIV-1) isolate LAI. The DB107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention of relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antilusogenic, antifusogenic, artivital or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The presents sequence represents one of the DP178-like/DP107-like peptides
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                                                                                                                                                  Identifying a compound that inhibits the formation of or disrupts a DP10/7/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex
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    Lawless MK, Merutka G;
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 71; 259pp; English.
Erickson JB,
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ilarity 80.0%;
Conservative
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AAR57812 standard; peptide; 6 AA.

(first entry)

93WO-JP01262.

93JP-0203962. 92JP-0238624

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Platelet; antithrombotic; inhibitor; cell adhesion; cancer; metastasis; extracorporeal circulation; coagulation; anticoagulant; cell fusion.
                                                                                                                        RGD contg. peptide having antithrombotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YAWA ) NIPPON STEEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-101121/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katada J, Sato Y;
                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1992;
18-AUG-1993;
                                                                               03-OCT-1994
                                                                                                                                                                                                                                                                                                   WO9405696-A
                                                                                                                                                                                                                                                                                                                                            17-MAR-1994.
                                                                                                                                                                                                                                                          Synthetic.
                                      AAR57812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a core polypeptide which may be linked to
an enhancer peptide to form a novel hybrid polypeptide. The hybrid
con polypeptide exhibits enhanced pharmacokinetic properties relative to
those exhibited by the core polypeptide when introduced into a living
system. It is used to increase the in vitro or ex vivo half-life of
the core polypeptide or the hybrid and core polypeptides can be used for
colled-coil peptide interactions. Other uses include preventing,
colled-coil peptide interactions that involving fusion of
interactions and viral infections that involve cell-cell and/or
infections) and viral infections that involve cell-cell and/or
colled-coil peptides equence increases the human
immunodeficiency virus, respiratory syncytial virus, Epstein Barr
virus, hepatitis B virus, Mason-Pfizer virus and polio virus).

The enhancer peptide sequence increases the half-life and reduces the
clearance rate of therapeutic peptides, which increases their efficacy
and minimises the incidence and severity of adverse side effects.

In addition, this increases the sensitivity of the diagnostic procedure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
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                                                                                                                                                                                                                                        Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatchropic; antiinflammatory; hybrid polypeptide; colled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merutka G, Anwer MK, Lambert DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.5%; Score 28; DB 22; Length 8; 80.0%; Pred. No. 6.4e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 51; 151pp; English.
                                                             AAB77919 standard; Peptide; 8 AA
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                                                                                                                                                      (first entry)
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                                                                                                                                                                                             Core polypeptide T1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guthrie KI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in which they are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TRIM-) TRIMERIS INC.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA;
                                                                                                                                                                                                                                                                                                                                                                                          WO200103723-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide -
                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1999;
                                                                                                                                                    19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barney S,
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                                                                                                        AAB77919;
                    RESULT 14
AAB77919
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NAMES OF COLOR COL

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The peptides given in AAR57801-28 have antithrombotic, anticoagulant and cell fusion inhibiting effects. They may be used in antithrombotic agents and as extracorporeal circulation coagulation inhibitors, cell adhesion inhibitors, cancer metastasis inhibitors and protecting agent in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
New peptides and their salts - used in platelet prepns., as antithrombotic agents and as inhibitors of e.g. cell adhesion, cancer metastasis and extracorporeal circulation coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.8%; Score 27; DB 15; Length 6; 50.0%; Pred. No. 6.4e+05; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 12, 2002, 17:14:32 Job time: 245 sec
                                                                                                                  Disclosure; Page 52; 88pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.85
Best Local Similarity 50.05
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                   (IC50 = 3.1 \times 10 -5 M).
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5 AAR57812 RESULT

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Sequence 22, Appl Sequence 21, App Sequence 919, App Sequence 91, Appli Sequence 9, Appli Sequence 9, Appli Sequence 28, Appli Sequence 28, Appli Sequence 38, Appli Sequence 19, Appli Sequence 225, Appli Sequence 225, Appli Sequence 225, Appli Sequence 226, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 11, Appli 
                                                                                                                 August 12, 2002, 17:12:17 ; Search time 20.43 Seconds (without alignments) 9.565 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-467-046-22
US-08-358-160-227
US-09-082-279B-919
US-09-158-572-9
US-09-28-174-9
US-09-28-174-9
US-08-014-426-28
PCT-US94-0119-28
US-08-014-426-28
PCT-US94-0119-28
US-08-462-661A-19
US-08-462-661A-19
US-08-525-539A-39
US-08-525-539A-39
US-08-358-160-225
US-08-358-108-111
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                              protein - protein search, using sw model
                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
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Match Length DB
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59
1 gywgkgyw 8
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length: 8
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Maximum DB
                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                     Run on:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,055
FILING DATE: 26-JUN-1992
PRIOR APPLICATION NUMBER: AU PUG621
FILING DATE: 26-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PUG622
FILING DATE: 26-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PUG623
FILING DATE: 26-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PUG624
FILING DATE: 26-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PUG644
FILING DATE: 26-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,901
FILING DATE: 26-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A

	8 6	24	40.7	œ (1 0	S-08	-233	-558	1-10		Sed	Sequence	10,	
	67	77	40.7			-08	-233	-558	7		Sedn	Sequence	25,	Ap
	30	7.7	40.7			us-08	-249	-371-7			Sedn	Sequence	7,	
_	31	24	40.7			S-08	US-08-160-604-28	-604	- 28		Sedn	Sequence	28,	Ap
	32	77	40.7			S-08	-160	-604	-29		Sedn	Sequence	29,	
	χ, c	47	40.7			s-08	- 586	-670	A-17	_	Sedn	Sequence	17,	
	ان 4 ت	7.7	40.7			s-09	-537	-357	-25		Sedn	Sequence	25,	
	3.5	77	40.7			CT-U	PCT-US95-06451-7	0645	1-1		Sedn	Sequence	,	Œ.
	36	23	39.0			s-08	-321	-625	-27		Sedn	Sequence	27,	Api
	37	23	39.0			S-08	-321	-625	-28		Sedn	Sequence	28,	
	38	23	39.0			8-09	-181	-083	-27		Sedu	Sequence	27	
	39	23	39.0			8-09	-181	-083	-28		Section	Sequence	200	
	40	23	39.0			60-5	US-09-258	-754	-167	~	200	Sections	167	
	41	23	39.0			50-5	113-09-042	-107-167	-167		500	Sequences	7 7	•
	42	23	39.0			118-07	0.0	-3340	2-5	. ^	מילום מילום	Sequence	2 5	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓
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		2 6	0.0			80.	-444	878-	-513	•	Sedn	Sequence	513	Ā
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						A	ALTCNMENTS	PINTS						
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	RESULT	1												
	US-08-467-046-22	-046-22	~1											
	; Sequence 22, Appli	e 22, A	Application US/0846704	On US/C	1846	7046								
	; Patent P	No. 594	18644											
	; GENERAI	L INFOR	GENERAL INFORMATION:											
	; APPL]	APPLICANT:	DOPHEIDE,	E, THEODORUS	DOR	JS AA	Æ							
	; APPL	APPLICANT:	FRENKEL,	, MAURICE		Ь								
	; APPL]	APPLICANT:	GRANT.	3	z									
	APPL	APPLICANT:	SAVIN	KETTH W										
	APPL	APPLITCANT.	_	M VODE	2									
	TTTT.	OF TR	TITLE OF INVENTION.		E GIN									
	NIIMBI	NIMBER OF S	SECTENCES.											
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	MET		READABLE FORM: TVDF: Flore: 41sk	FORM:	د									
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	100	ODERATING	SYSTEM TO COMPACED TO SAGE	DC-DOG AG-DOG	770	7) 2	r.							
	SOS	SOFTWARE:		PatentIn Release	1 0 0	#103		Version		#1 25				
	CURRE	INT APP	1	DATA)			1101		•				
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Gaps
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.5%; Score 28; DB 1; Length 4; Best Local Similarity 100.0\%; Pred. No. 1.7e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8;
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Pred. No. 1.7e+05;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-315-304B-919
; Sequence 919, Application US/09315304B
; Patent No. 6348568
                                    REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEFAN 202-737-3528
TELEFAX: 24863
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 919, Application US/09082279B Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COTHER INFORMATION: Core polypeptide US-09-082-279B-919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-09-082-279B-919
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| Sequence 227, Application US/08358160
| Patent No. 5663143
| Sequence 227, Application US/08358160
| Patent No. 5663143
| GENERAL INFORMATION:
| APPLICANT: LEY, Arthur C. APPLICANT: LADNER, Robert C. APPLICANT: GUTERWAN, Sonia K. APPLICANT: GUTERWAN, Sonia K. APPLICANT: MARKAND, William APPLICANT: MAILS Bruce L. APPLICANT: MAILS BROWE BROWN ROUNDERED HUMAN-DERIVED KUNITZ
| TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE INWABER OF SEQUENCES: 234
| CORRESPONDENCE ADDRESS: 324
| CORRESPONDENCE ADDRESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: US/08/33,31
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/009,319
FILING APPLICATION NUMBER: US 08/009,319
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/487,063
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGGMT INFORMATION:
                                                                                                                                                                                                                                                                                                                              | LENGTH: 8 maino acids | LENGTH: 8 maino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: peptide | FRAGEMENT TYPE: internal | CRIGIMAL SOURCE: | ORIGIMAL SOURCE: | ORGANISM: Trichostrongylus colubriformis US-08-467-046-22
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELERAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7*
Matches 4; Conservative
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US-08-358-160-227
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Score 26; DB 1; Length 6; Pred. No. 1.7e+05; 1; Mismatches 0; Indels
          A4.18;
Similarity 75.08;
3; Conservative 1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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                          Best_Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 4; Conserv
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                                                                                    1 gywg 4
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            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/O7/718,577
FILIG DATE: 19910620
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One Market Plaza, Steuart Street
Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DOWER, William J.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
TITLE OF INVENTION: SCREENING SYSTEMS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROR APPLICATION 439

PROR APPLICATION NUMBER: US 07/541,108

FILING DATE: 20-UNU-1990

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 30,23

REFERRENCE/DOCKET NUMBER: 11509-25-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 326-2400

TELEFAX: (415) 326-242

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                      CURRENT APPLICATION NUMBER: US/09/315,304B
                                  CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 8
                                                                                                                                                                                                                              ; OTHER INFORMATION: Core polypeptide US-09-315-304B-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07718577
Patent No. 5432018
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          47.5%;
                                                                                                                                                                                                                                                                                                Query Match 4/...
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-718-577-2
FILE REFERENCE: 7872-052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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3 WGYGY 7
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US-07-718-577-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                               NS-09-258-754-9
Sequence 9, Application US/09258754
Factor No. 6174687
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P.LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT APPLICATION NUMBER: 09/042,107
EARLIER FILING DATE: 1999-02-26
SEALIER PILING DATE: 1998-03-13
NUMBER OF SED ID NOS: 452
SOFTWARE: PATENTIN OF SED ID NOS: 452
SOFTWARE: PATENTIN OF SED ID NOS: 452
SED ID NO 9
SED ID NO 9
SED ID NO 9
SED ID NO 9
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.1%; Score 26; DB 4; Length 7; 80.0%; Pred. No. 1.7e+05; Live 0; Mismatches 1; Indels
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Sequence 9, Application US/08232261
Patent No. 5498601
GENERAL INFORMATION:
APPLICANT: Sato, Yoshimi
APPLICANT: Ratada, Jun
TITLE OF INVENTION: Aggregation-Inhibiting Agents, Blood
TITLE OF INVENTION: Coagulation-Inhibiting Agents, Blood
TITLE OF INVENTION: Circulation, Cell Adhesion-Inhibiting Agents, Tumor
TITLE OF INVENTION: Mestastasis-Inhibiting Agents...
NUMBER OF SQUENCES: 14
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.1%; Score 26; DB 5; Length 8; 42.9%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mr. Edward W. Greason, Kenyon & Kenyon
                                                      1; Mismatches
                                                                                                                                                            CORRENT AFFLICATION DATA:

CLASSIFICATION NUMBER: PCT/US94/01319
FILING DATE: 04-FEB-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,426
FILING DATE: 05-FEB-1993
ATTORNEY/AGENT TREORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 5490A-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-240
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Mr. Edward
STREET: One Broadway
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Best Local Similarity
Matches 3; Conserv
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1 HWYNEYW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-232-261-9
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                                                                                Sequence 28, Application US/08014426

Patent No. 5512435
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benschler, Markus F.
APPLICANT: Bratt, Ramesh
APPLICANT: Bratt, Ramesh
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
COUNTY. California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Remeabler, Markus F.
APPLICANT: Boat, Remeable
APPLICANT: Bhatt, Remeable
APPLICANT: Bhatt, Remeable
APPLICANT: Dower, William
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: PEPTIDES
TORRESPONDENCES: 65
CORRESPONDENCES: 65
CORRESPONDENCE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/014,426
FILING DATE: 05-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26; DB 1; 1
Pred. No. 1.7e+05;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION UNDRER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEPHORE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US94-01319-28
; Sequence 28, Application PC/TUS9401319
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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Best Local Similarity
Matches 3; Conserv
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                                                                        US-08-014-426-28
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Gaps
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Patent No. 5747447

GENERAL INPORMATION:
APPLICANT: BANDATION:
APPLICANT: BUNDOLH, ANNE
TITLE OF INVENTION: STABLE POLYPEPTIDE COMPOSITION
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: Plue Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                              Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%; Score 25; DB 6; Length 6; 80.0%; Pred. No. 1.7e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                      RESULT 12
5318899-55
;Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
FILING DATE: 16-JUN-1989
SEQ ID NO:55:
                                                                          Score 25; DB 1; ]
Pred. No. 1.7e+05; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/055,636
FILING DATE: 30-APRIL-1993
APPLICATION NUMBER: US 07/876,625
FILING DATE: 30-APRIL-1992
                                                                          42.4%;
80.0%;
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Best Local Similarity 80.0*
                                                                                                                 Conservative
                                                                          Query Match
Best Local Similarity
Matches 4; Conserva
       cyclic
     ; TOPOLOGY:
US-08-462-661A-38
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5318899-55
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Pred. No. 1.7e+05;
"...matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/08462661A
Fatent No. 5747447
GENERAL INFORMATION:
APPLICANT: SWIFT, ROBERT L.
APPLICANT: BUNDCLP, ANNE
TITLE OF INVENTIONS: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: Five Palo Alto Square, 3000 El Camino Real
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/055,636
FILING DATE: 30-APRIL-1993
APPLICATION NUMBER: US 07/876,625
FILING DATE: 30-APRIL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD L. NEELEY, Ph.D.
REGISTRATION NUMBER: 30,092
REFERENCE/DCOKET NUMBER: CORT-003/08US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,661A
FILING DATE: 5-UUNE-1995
CLASSIFICATION: 530
           RECISTRATION NUMBER: 34,297
REFERENCE/DOCKET NUMBER: 2002/001
TELECOMMUNICATION INFORMATION:
TELEPHANE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEFAX: (212) 425-5288
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acid
                                                                                                                                                                                                                                                                       ; ORIGINAL SOURCE:
; ORGANISM: N/A (synthetic)
US-08-232-261-9
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415)843-5000
TELEFAX: (415)857-0663
Bonham, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                         ANTI-SENSE: NO
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US-08-462-661A-38
                                                                                                                                                                                                TOPOLOGY:
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| WGRG 4
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; SEQ ID NO:41:
; LENGTH: 8
5318899-41
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APPLICANT: CERIANI, ROBERTO L.
APPLICANT: ETERSON, JERRY A.
TITLE OF INVENTION: MESCOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MESTANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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42.4%; Score 25; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: /note= "This position is C-NH2." US-08-462-661A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATORNEZ/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 494-0792
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD L. NEELEY, Ph.D.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: CORT-003/08US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)843-5000
TELEPEAX: (415)857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08525539A Patent No. 6309636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site LOCATION: 8
                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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US-08-525-539A-39,
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US-08-525-539A-39
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CITY: Pal
STATE: CA
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  42.4%; Score 25; DB 4; Length 8; 50.0%; Pred. No. 1.7e+05; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.4%; Score 25; DB 6; Length 8; 80.0%; Pred. No. 1.7e+05; live 0; Mismatches 1; Indels
                                                                                                                                                                                  RESULT 15
5318899-41
; PALENT NO. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.; WOLF, DAVID L.; CHARO,
; STAREL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 83
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/483,229
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 418,028
FILING DATE: 06-OCT-1989
APPLICATION NUMBER: 367,509
FILING DATE: 16-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 12, 2002, 17:14:59 Job time: 162 sec
Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                       1 WDGDYW 6
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2002, 17:18:51; Search time 24.99 Seconds (without alignments) 30.761 Million cell updates/sec

10-071247-2 66 1 cywgcgyw 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

603 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ð			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	73	34.8		4	I79564	hypothetical TCL3
7	20	0		~	JH0253	qut pentapeptide -
m	19	8	9	7	F41946	T-cell receptor da
4	19	æ	80	~	S19288	ase - Kluvo
5	18	7.	9	7	A41946	ď
9	18	27.3	7	7	B33882	Ε
7	18		7	7	533567	tubulin beta-3 cha
80	17	ď.	4	7	B53284	eceptor
σ	17	S.	9	7	A61068	akinin - m
10	17	'n.	9	~	PT0629	Į,
11	17	25.8	9	7	PT0637	receptor
12	17	5.	7	7	S57274 .	lalveerol
13	17	25.8	7	7	PT0628	T-cell receptor he
14	17	2	7	7	PT0642	1 receptor
15	17	25.8	7	7	PT0722	l receptor
16	17	2	7	~	PT0586	l receptor
17	17	2	7	7	PT0728	-cell receptor
18	17	2	7	7	B48394	fat-qlobul
19	17	2	7	~	PD0029	
20	17	Ω	80	7	A31570	in-co
21	17	5.	œ	7	JS0315	leucokinin V - Mad
22	17	5.	æ	~	JS0316	IA
23	17	'n.	80	N	JS0317	- IIA
24	17	25.8	8	~	JS0318	
25	17		80	7	PT0724	- a
56	16	4	3	٣	A22565	-phycoerythrin
27	16	24.2	2	7	F22565	
28	15		2	~	A33882	
29	15	22.7	S.	7	S65726	н

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Gaps ;

Query Match
30.3%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels

6 gyw 8 |:| 1 GFW 3

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glycoprotein compo T-cell receptor be	venom heptapeptide Ig beavy chain Opp	cerebellar degener	mabinlin II chain	Ig mu chain D regi	acetylcholinestera globulin IV alpha	ameletin - rat	dermorphin - Rohde	iatty-acia synthas glutathione transf	dermorphin (Lys-7)	
H48394 PT0532	A58512 PT0278	B35640	S38516	E33932	A41117 S09478	A61411	A61324	S71870	S36662	S59622
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22.7	22.7	21.2	21.2	21.2	19.7	19.7	19.7	19.7	19.7	19.7
15 15	15 14	14	14	14	13	13	E E	13	13	13
30	32 33	34 35	36	37	9 G	40	41	43	44	45

ALIGNMENTS

	RESULT 1
	hypothetical TCL3 protein (mistranslated) - human (fragment)
	C; Species: Homo sapiens (man)
	C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
	C; Accession: 179564
	Kizutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.
	Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990
	A) 11LLE: The (1(10):14) (9/44) (1/10):14) of T-cell acute lymphoblastic leukemia juxtaposes the
	A; Accession: 179564
	A; Status: translation not shown; translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
_	A; Residues: 1-6 <zut></zut>
	A;Cross-references: GB:M33602; NID:g339907; PIDN:AAA66449.1; PID:g807656 C:Comment: This is the hypothetical translation of a common translation of a
_	ייני בייני ב
	Dest Docal Similarity 73.0%; Fred. NO. 2.88+U); Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	QY 3 wgcg 6
	Db 2 WCG 5
	RESULT 2
	0.000
	our peniapetriae dapanese eei
	C. Species: Angulila Japonica (Japanese eel)
	<pre>c.race. 11 mail 1392 *sequence_revision 31-Mail-1992 *text_change 11-Apr-1995 C:Accession: JH0353</pre>
	R;Uesaka, I.; Ikeda, I.; Kubota, I.; Muneoka, Y.: Ando. M.
	Biochem. Biophys. Res. Commun. 180, 828-832, 1991
	A. M.
	A.Mccession: JH0253; MUID:92062113 A.Mccession: JH0353
	A; Molecule type: protein
	A.Residues: 1-5 (UES)
	A paper intended to the comment. This peptide increased hasal tone of the circular muscle of the comment. This
	, and of the circular muscle of the gastro-intestinal junction.
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10-071247-2.closed.rpr

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T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, Nu; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Reference number: A53284; MUID:91342695
A;Accession: B53284
A;Accession: B53284
A;Molecule type: DNA
                                                                                                                                                                                                                                                                       caddium-binding heptapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: B33882
R;Jackson, P.J; Unkefer, C.J; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan A;Reference number: A94182; MUID:88016144
A;Accession: B33882
A;Molecule type: proctein
A;Residues: 1-7 <JA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 18; DB 2; 140.0%; Pred. No. 2.8e+05; iive 1; Mismatches 2.
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A;Cross-references: FlyBase:FBgn0003888
A;Introns: 5/3
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Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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2 ywgcgy 7
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A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
R;Whetsell, M.: Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946
A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                           R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gg A;Reference number: A41946; MUID:92049316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orginate - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem, J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from language number: S19288
A;Reference number: S19288
A;Reference number: S19288
A;Accession: S19288
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                                                                                                                                                                   C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-6 <WHE> C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.8%; Score 19; DB 2; Length 8; 50.0%; Pred. No. 2.8e+05; Lindels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 2; Length 6;
Pred. No. 2.8e+05;
0; Mismatches 2; Indels
                                                                                                                             T-cell receptor gamma chain (la.27) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.8%;
Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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Cypecies: Psychrobacter immobilis
Cybecies: Psychrobacter immobilis
Cybecies: Psychrobacter immobilis
Cybecession: S57274
Ryarpigny, J.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
A; Fitle: Corrigendum to "Cloning, sequence and structural features of a lipase from the A; Reference number: S57274; MUID:95359197
A; Accession: S57274
A; Molecule type: DNA
                                                                                                                                                                                                     cell receptor beta chains have few N regions
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J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A; Reference number: PT0509; MUID:91277601
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                                             C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Date: 17-711-1992 #sequence_revision 17-711-1992 #text_change 30-May-1997
C.Accession: PT0637
R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few A.Reference number: PT0509; MUID:91277601
A.Accession: PT053
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A.Accession: PT053
A.Accession: PT053
A.Accession: PT053
A.Status: translation not shown
A.Status: translation not shown
A.Status: Learning and A.Status: C.S.E.
A.Status: T.C.E. Source: newborn thymus, strain BALB/C
C.Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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C; Keywords: T-cell receptor
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A;Cross-references: EMBL:X67712
C;Keywords: carboxylic ester hydrolase
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A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
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Best Local Similarity 100.
Matches 2; Conservative
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J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
A; Accession: PT0629
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A61068
A61068
Locustakinin - migratory locust
C;Species: Locusta migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C;Accession: A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A. Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, A;Reference number: A61068; MUID:92262851
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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A;Residues: 1-6 <SCH>
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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                    A;Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-6 < FE2>
A; Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C; Keywords: T-cell receptor
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25.8%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.8e+05;
Live 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
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Best Local Similarity 100.0
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Best Local Similarity 100.0
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A; Residues: 1-4 <HAR>
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Trocal receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Decies: Mus musculus (house mouse)
C; Decies: Mus musculus (house mouse)
C; Accession: PT0722
B; Feeney, A.J.
C; Accession: PT0722
B; Feeney, A.J.
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
A; Reference number: PT0722
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-7 KFES
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0; Indels
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 Best Local Similarity 100.
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5 WG 6
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August 12, 2002, 17:20:43 ; Search time 13.13 Seconds (without alignments) 23:592 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                       105224 seqs, 38719550 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P					
Result		Query					
No.	Score	Match	Match Length DB	DB	ID	Description	tion
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-	7	72.8	9	_	LOK1_LOCMI	P41491 locusta	locusta
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	Description	P41491 locusta mig	691	leucopha		7	3.1	7	Н	. ,	_	_	-		P30369 macropus eu	bothrops			achatin	P35920 achatina fu		P14086 gryllus bim		P25423 melolontha	P14595 tabanus atr	<u>~</u>	P04549 periplaneta	6	P81707 brassica na	P08939 pandalus bo	P81780 herpes simp	P58648 octopus min	P81864 pardachirus	P82073 litoria rub
	ID	LOK1 LOCMI	ACI_THUAL	LCK1_LEUMA	LCK2_LEUMA	LCK3_LEUMA	LCK4_LEUMA	LCK5_LEUMA	LCK6_LEUMA	LCK7_LEUMA	LCK8_LEUMA	OCP3_OCTMI	UF01_MOUSE	ALL5_CYDPO	CCKN_MACEU	- 1	- 1	- 1	WWA1_ACHFU	WWA2_ACHFU	WWA3_ACHFU	AKHG_GRYBI	AKH_LIBAU		AKH_TABAT	HTF1_PERAM	HTF2_PERAM	HTF_TENMO	PLP_BRANA	RPCH_PANBO	VGLG_HSV2B	OCP1_OCTMI	PAP2_PARMA	RE32_LITRU
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æ	Query Match	25.8	25.8										ď	٠.	18.2	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	۰	16.7	٠,	٠	٠.	16.7		•	15.2	15.2
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
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01-NOV-1990 (Rel. 16, Last annotation update)
Nol-NOV-1990 (Rel. 16, Last annotation update)
Angiotensin-converting enzyme inhibitor.
Thunnus albacares (Tellowfin tuna) (Neothunnus macropterus).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostoni;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Scombridae: Thunnus.
NCBI_TaxID-8236;
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SEQUENCE.

34 10 15.2 8 1 UPOG_MOUSE P36644 mus musculu											
34 10 15.2 8 1 UFGG_MOUSE P98644 mus mm s 35 9 13.6 4 1 ACH_ACHEU PR2994 achat. 37 9 13.6 6 1 ACH_ACHEU PR2994 achat. 38 9 13.6 8 1 ACH_ACHEU PR2994 achat. 39 9 13.6 8 1 ACH_ACHEU PR2994 achat. 30 9 13.6 8 1 CHR_BUNAN P0177 homo s 41 8 12.1 3 1 CRAM_HINAN P0177 homo s 42 12.1 4 1 DCML_DEECH PR295 or 43 12.1 7 1 TANA_HINAS P0177 homo s 44 8 12.1 7 1 TANA_HINAS P0177 homo s 44 12.1 7 1 TANA_HINAS P0177 homo s 44 12.1 7 1 TANA_HINAS P0177 homo s 44 12.1 7 1 TANA_HINAS PR25 or 44 12.1 7 1 TANA_HINAS PR25 or 44 13.1 7 1 TANA_HINAS PR25 or 44 14.3 8 12.1 7 1 TANA_HINAS PR25 P018 P01875 pinus 45 12.1 7 1 TANA_HINAS PR25 P018 P01875 pinus 46 12.1 7 1 TANA_HINAS PR25 P018 P01875 pinus 47 14.4 1.1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ulu fu ars ars ien es ien ien nas edi nas							z	0;		
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NCBI_TaxID=6988;
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-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINGUT).
-!- SIMILARITY: TO THE OPHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holman G.M., Cook B.J., Nachman R.J.; "Isolation, prinary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
                                          Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura "Isolation of angiotensin-converting enzyme inhibitor from tuna
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin II (L-II).
Leucokinin II (L-II).
Leucophaea maderae (Madeira cockroach).
Rukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Orthopteroidea; Blaberoidea; Blaberidae; Leucophaea.
NCBI_TAXID=6988;
                                                                                                                                                                                                          25.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05; 1ive 0; Mismatches 0; Indels
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Blochem. Blophys. Res. Commun. 155:332-337(1988).
PIR. A1570; A31570.
SEQUENCE 8 AA: 953 MW; 6AA863733051F1B7 CRC64;
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01-MAY-1991 (Rel. 18, Last sequence update)
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                      MEDLINE-88326322; PubMed-3415688;
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MOD_RES 8 8
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| SEQUENCE, AND SYNTHESIS.
| TISSUE=Head;
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Matches 2; Conserv
TISSUE-Muscle;
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P21140;
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Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                        Comp. Biochem. Physiol. 84C:205-211(1986).
-!- FUNCTION: THIS CEPHALDMOYTRODIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
        "Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.",
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01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin IV (L-1V).
Leucophaea maderae (Madeira cockroach).
Eucophaea maderae, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Plaberoidea; Blaberidae; Leucophaea.
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Leucokinin III (L-III).
Leucophaea maderae (Madeira cockroach).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
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        MOD_RES
        8
        AMIDATION.

        SEQUENCE
        8 AA; 910 MW; DC6365B449C866DA CRC64;

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100.0%; Pred. No. 1e+05;
Live 0; Mismatches (
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01-MAY-1991 (Rel. 18, Last sequence update)
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Holman G.M., Cook B.J., Nachman R.J.;
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MOD_RES 8 8
SEQUENCE 8 AA; 852 MW;
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Neuropeptide; Amidation.
MOD_RES 1 1 1 1 MOD_RES 8 8 8 SEQUENCE 8 AA; 935 MW;
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Best Local Similarity
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P19989;
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SEQUENCE
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LCK8_LEUMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure, and synthesis of leucokinins V and VI:

"Isolation, primary structure, and synthesis of leucokinins V and VI:

myotropic peptides of Leucophaea maderae.";

comp. Biochem. Physiol. 88C:27-30(1987).

-I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINGUT).

-I- SIMILARITY: TO THE OTHER LEUCOKININS.

PIR; JS0315; JS0315.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   STIMULATES CONTRACTILE
                             Holman G.M., Cook B.J., Nachman R.J.;
"Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of cephalomytropins.";
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0
                                                                                                                                                                                                                                                                                                                                  Leucokinin V (L-V).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Neopiera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                         0; Indels
                                                                                                                                                                    Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 1; Length 8; Pred. No. 1e+05; 0; Mismatches 0; Indels
                                                                                                                         8 8 AMIDATION.
8 AA; 906 MW; DC6365B1E9D5BDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 8 AMIDATION.
8 AA; 784 MW; 736365A5B9C865B8 CRC64;
                                                                                                                                                                  Score 17; DB 1;
Pred. No. 1e+05;
0; Mismatches (
                                                                      Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE ST
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leucokinin VI (L-VI).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA.
                                                                                                                                                                                                                                                                                   8 AA.
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.8%; Scut-
100.0%; Pred
0; }
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                                                                                                                                                                Query Match 25.8%; Scc
Best Local Similarity 100.0%; Pi
Matches 2; Conservative 0;
                                                                                                               Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.
MOD_RES 8 8
SEQUENCE 8 AA: 784 MWJ
          SEQUENCE, AND SYNTHESIS. TISSUE=Head;
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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les 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Head;
                                                                                                                                                                                                                                                                                LCK5_LEUMA
P19987;
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P19988;
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Best Local S
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LCK5_LEUMA
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LCK6_LEUMA
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                                                                                                                                                            MEDLINE-87052651; PubMed-2877794;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman R.J.;
Hisolation, primary structure, and synthesis of leucokinins V and VI:
myotropic peptides of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:27-30(1987).
-I-FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-I-SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
HELLOTHIS ZEA ADIPOKINETIC HORMONE.
PIR; 30316; JS0316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberoidea; Laberidae; Leucophaea.
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Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 8 AMIDATION.
8 AA, 935 MW; 9D6365B1E9D5A5A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
DC6365A5B9CDC76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
101-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VII (L-VII).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 866 MW;
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5 AA.

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TISSUE-Fibroblast;
MEDLINE-55009907: Pubmed-7523108;
MEDLINE-55009907: Pubmed-7523108;
MEDLINE-55009907: Pubmed-7523108;
MEDLINE-55009907: Pubmed-7523108;
MEDLINE-55009907: Pubmed-7523108;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
Electrophoresis 15:735-745(1994).
Electrophoresis 15:735-745(1994).
PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                 Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 15; DB 1; Length 66.7%; Pred. No. 1e+05; ive 0; Mismatches 1; Inde
                                                                                                                                                                                                                                                                                                                                                                                                          5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.7
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.7
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                        STANDARD;
                                                                                                                                                                                   (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
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                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALL5_CYDPO
P82156;
                                                                                     UF01_MOUSE
P38639;
GSW 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 gyw 8
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SEQUENCE
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                                                          MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                           Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure and synthesis of leucokinins VII and
"Isolation, primary structure and synthesis of leucokinins VII and
VIII: the final members of this new family of cephalomyotropic
peptides isolated from head extracts of Leucophaea maderae.";

comp. Biochem. Physiol. 88C:31.34(1987).

-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-!- SIMILARITY: TO THE OTHER LEUCOKININS.

PIR; JS0318; JS0318.

Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
02-MAR-2002 (Rel. 41, Last annotation update)
03-MAR-2002 (Rel. 41, Last annotation update)
03-MAR-2003 (Octopus, Melazoa, Wollusca; Cephalopoda; Coleoidea; Octopoda;
10-MAR-2003 (Melazoa, Mellusca; Octopodidae; Octopoda;
03-MAR-2003 (Melazoa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less
                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBL_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.7%; Score 15; DB 1; Length 4; 66.7%; Pred. No. 1e+05; 1; Indels 1; or Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 2 D-SERINE (IN OCP-4).
4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   8 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 17; DB 1;
100.0%; Pred. No. 1e+05;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VIII (L-VIII).
Leucophaea maderae (Madeira cockroach).
8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     active than Ocp-3.
SUBCELLULAR LOCATION: Secreted
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides 21:623-630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-amino acid.
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ses 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                               TISSUE=Head;
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P58649;
 LCK8_LEUMA
P19990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wg 4
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Duve H., Johnsen A. H., Maestro, J. L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.; Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).

-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%; Score 13; DB 1; Length 8; 100.0%; Pred. No. 1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AMIDATION.
898 MW; 922879CABB58640D CRC64;
                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 5.
8 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                     Cydia pomonella (Codling moth).
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BPP7_BOTIN
ID AC 73042;
DT 01-REP1993 (Rel. 25, Created)
DT 01-REP1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE madykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidosuuria; Squamata; Scleroglossa; Serpentes; Colubroidea; OX Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cintra A.C.O., Vieira C.A., Giglio J.R.;
"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
-1. Function: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGIOTENSIN CONVERTING ENTYME AND ENHANCES THE ACTIVITY OF BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT. IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                       Peptides 9:429-431(1988).

-!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
IN THE BRAIN IS NOT CLEAR.

-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A430011. A430012.
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
ANDLARS
MOD_RES
MOD_RES
MOD_RES
MAIDATION.
                                                                                                                                     Macropus eugenii (Tammar wallaby), and Dasyurus viverrinus (Southeastern quoll). Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus. NCBL_TaxID=9315, 9279;
                                                                                                                                                                                                                                                                                Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
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DDCAA68378768B5A CRC64;
                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Cholecystokinin (CCK).
                                8 AA.
                                PRT;
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SEQUENCE.
TISSUB-Venom;
MEDLINE-90351557; Pubmed=2386615;
                                                                                                                                                                                                                                                               MEDLINE=88234141; PubMed=3375140;
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Similarity 66.7%;
2; Conservative (
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                              STANDARD;
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TISSUE=Brain;
                             CCKN_MACEU
P30369;
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                             1 1 PYRROLIDONE CARBOXYLIC ACID. 5 AA; 629 MW; 776DC37326B00000 CRC64;
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             Hypotensive agent; Venom.
MOD_RES 1 1
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Q64971 alfalfa mos
Q9572 shigella dy
Q95213 oryctolagus
P82096 litoria rub
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didelphis m
macropus eu
choloepus h
                                                            Q95945 saccharomyc
P82065 litoria rub
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myrmecophag
erinaceus c
talpa altai
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sorex arane
echinops te
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drosophila
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDIINE-96377339; PubMed-8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 6; Length 8;
Pred. No. 5.6e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Evidence for insufficient chondrocytic differentia
of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL: S83371; AAD14433.1; -.
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8 AA; 1028 MW; B859C7272EA77371 CRC64;
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Compugen Ltd.
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          GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 1008
Listing first 45 summaries
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01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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MOD_RES 8 8
SEQUENCE 8 AA; 909 MW;
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                                              PRELIMINARY;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HMG-1-LIKE PROTEIN (FRACMENT).
HMG-1-LIKE PROTEIN (FRACMENT).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimtophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
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                                                                                                                                                                        Laux T., Goldberg R.B.; "A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
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TISSUE-CORPORA CARDIACA;

MEDLINE-98010462; PubMed-9350979;

Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

Predel R., Rituctural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
KININ-1 (PEA-K-1).
Periplaneta americana (American cockroach).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Blattaida;
NCBL_TaxID=6978;
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Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
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                                                                                                                                              STRAIN-CV. ESSEX; TISSUE-ROOT;
MEDLINE-91367679; PubMed*1891369;
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MOD_RES 8 8
SEQUENCE 8 AA; 950 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                              KININ-2 (PEA-K-2).

Periplaneta americana (American cockroach).

Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

Blattcidea; Blattidae; Periplaneta.

NCBI_TaxID=6978;
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-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      americana.";
Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
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                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Pred. No. 5.6e+05;
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MEDLINE=98010462; PubMed=9350979;
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Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
"Small subunit of the mammalian mitochondrial ribosome. Identification
of the full complement ribosomal proteins present.";
Submitted (DEC-2000) to the SWISS-PROT data bank.
-! SUBCELULAR LOCATION: MITOCHONDRIAL.
Ribosomal protein; Mitochondrion.
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STRAIN-KN T96-0620, S-1058, AND CL 68578;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065068; AAD03668.1; -.
EMBL; AF065066; AAD03668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bovidae; Bovinae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

MCBI_TaxID=9913;
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NCBI_TaxID=85755;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
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Last annotation update)
             C76365B449CDC775 CRC64;
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                                                                      25.8%; Score 17; DB 5; Lo 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0;
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100.0%; Pred. No. 5.6e+05;
Live 0; Mismatches 0;
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             865 MW;
                                                                                                                    Conservative
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MEDLINE-98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
Prolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RININ-5 (PEA-K-5).
Periplaneta americana (American cockroach).
Periplaneta mericana (American cockroach).
Pukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Periplaneta, Orthopteroidea; Dictyoptera; Blattaia; MCBL_TaxID-6978;
                                                                                                                                                                                                                                                                                                                 Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Nooptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
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-1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
-1- SIMILARITY: BELONGS TO THE KININ FAMILY.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;
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100.0%; Pred. No. 5.6e+05;
tive 0; Mismatches 0;
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    Conservative
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Best Local Similarity
'-hag 2; Conserva
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
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MEDLINE=21429115; PubMed=11543634;
Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
Watanabe K., Tanaka T.;
"The human mitochondrial ribosomal protein genes: Mapping of 54 ge
to the chromosomes and implications for human disorders.";
Genomics 77:65-70(2001).
EMBL; AB051346; BAB54936.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL, 132083, AAA73880.1; -.
NON_TER 8 8 8
                            24.2%; Score 16; DB 12; Length 7; 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL RIBOSOMAL PROTEIN L39 (FRAGMENT).
                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(CLONE XP19G12A) (FRAGMENT).
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Best Local Similarity 100.
Matches 2; Conservative
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               Ouery Match
Best Local Similarity
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CTAMAOCA-Mikaza LK., Nang R.N., Schnurr D.P.;
CTAMAOCA-Mikaza LK., Nang R.N., Schnurr D.P.;
Wolecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065064; AAD03659.1; --
EMBL; AF065063; AAD03659.1; --
EMBL; AF065063; AAD03659.1; --
                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=28280;
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Viruses; dsDNa viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=10519;
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MEDLINE-GOMEN;
MEDLINE-9175282; PubMed-10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
Crawford and variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";
J. Clin. Microbiol. 37:1107-1112(1999).
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065; AAD03662.1; ...
1 1 1 SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA; 980 MW; 7B5EA414140322A0 CRC64;
             DB 12; L
. 5.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%; Score 16; DB 12; I 100.0%; Pred. No. 5.6e+05; ative 0; Mismatches 0;
7 AA.
                                                                                                                                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                            Q9YIQ9 PRELIMINARY;
Q9XIQ9;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-OCT-2001 (TrEMBLrel. 18, L
PVI CORE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVI CORE PROTEIN (FRAGMENT).
                                                           2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Human adenovirus type
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Best Local Similarity
Matches 2; Conserv
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SEQUENCE FROM N.A.
                                       Best Local Similarity
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6 Cx 7
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6 cy 7
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SEQUENCE
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Q9YVE3;
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                                                           Matches
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Q9Y IQ9
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Gaps

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54 genes

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Search completed: August 12, 2002, 17:20:24 Job time: 346 sec
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Best Local Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Receptor.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Burosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=96198747; PubMed-8612486;
YOShikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-ROOT;
MEDLINE-21171025; PubMed=11277426;
MEDLINE-21171025; PubMed=11277426;
MEDLINE-21171025; PubMed=11277426;
Mercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
"Arabidopsis thaliana genes expressed in the early compatible interacion with root-knot nematodes.";
MOI. Plant Microbe Interact. 14:288-299(2001).
BMBL; AJ286350; CAB71014.2;
Hypothetical protein.
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                                                                 Length 8;
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Last annotation update)
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Last annotation update)
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                                                      24.2%; Score 16; DB 4; Le
100.0%; Pred. No. 5.6e+05;
Live 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
HYPOTHETICAL 0.7 KDA PROTEIN (FRAGMENT).
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
ORPHAN RECEPTOR TR4-NS (FRAGMENT).
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                                                                                                                               Conservative
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                                                          Query Match
Best Local Similarity
Matches 2; Conserv
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SEQUENCE FROM N.A.
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090583
AC 090583
DT 01-JUN
DT 01-DUN
DT 01-DUN
DT 01-DCM
GN DIDD 11
OS ATABDÍGO
CC EUKATY
CC EUCALY
NN I 1
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055184
AC 055184
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DT 01-JUN
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GN TR4.
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CC EUKATY
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Gaps
                                                        Yoshikawa T., DuPort B.R., Leach R.J., Detera-Wadleigh S.D.; "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene."; Genomics 35:361-366(1396).

EMBL; U59454; AAB914331; -.
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SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
STRAIN-SPRAGUE-DAWLEY;
MEDLINE=96299786; Pubmed=8661150;
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AAY03715
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3: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1981.DAT:*
4: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1982.DAT:*
5: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1982.DAT:*
5: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1985.DAT:*
6: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1980.DAT:*
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19: /SIDS1/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                            747574 seqs, 111073796 residues
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                                                                                                                    August 12, 2002, 17:14:32;
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Somatostatin deriv Somatostatin deriv Neuromedin B and s Neuromedin B and s Immunogenic peptid (F-18) (F-18) Immunogenic peptid Fluorine-18 (F-18) Fluorine-18 Fluorine-18 AAY03715 AAY76817 AAY03714 AAY03716 AAY42918 AAY42915 AAB59640 AAY76818 AAB59641 AAB59641

11-MAR-1999

Neuromedin Band s Biostatin TT232 sy

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7 13 AAR27179 7 15 AAR56817 7 18 AAW18456	19 AAY22 19 AAY18 19 AAW51	19 AAW50 19 AAW45	20 AAY42	20 AAY42 20 AAY42	20 AAY42	20 AAY42	20 AAY42	20 AAY42	20 AAY42	20 AAY42	20 AAY25	21 AAB19	21 AAB24	21 AABU/	21 AAYS1	21 AAY81	22 AAU08	22 AAB59	22 AAB59	22 AAB59	22 AAB59	22 AAB59	22 AAB91	22 AAB59	22 AAB59	CHICLIAN
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ALIGNMENTS

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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                               /note= "N-terminal acetylation; optionally has a free or protected thiol group"
                                                                                                                                                                                                                                                                                                                                                              "D-form residue; optionally has a free or protected thiol group"
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                                                                                               Fluorine-18 (F-18) labeled peptide 2.
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AAY03715 standard; peptide;
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                                                                08-JUN-1999
                                                                                                                                                                                 Synthetic
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Misc-difference
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                                                                                                                                                                                                 22-JUN-1998;
                                                                                                                                                                                                             14-0CT-1998;
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                                                                                                                                                 29-DEC-1999
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ω
                                                                                                                                                                                                                                                                                                                             conjugates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY03714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                               The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron emission temporaphy. Radiolabeling thiol-containing peptides with canisated alkene in which at least one of the two double bonded a fluorinated alkene in which at least one of the two double bonded a fluorinated alkene in which at least one of the two double bonded a rabon at least one leaving group comprising 1. Br. Cl. azide, tosylate, mesylate, mesylate, nosylate, nosylate, mesylate, mesylate, mesylate, mesylate, riflate. h. m = 0-2; n+m = 0-2; X = 1, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, maleimide of principally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl. R2 = I, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, maleimide of your carid, tertiary amine, quaternary ammonium, alkyl.

Sr. Cl. azide, tosylate, mesylate, nosylate, triflate, maleimide or quaternary ammonium, alkyl.

Coptionally substituted by CONH2, COOH, OH, sulfonic acid, tertiary amine or quaternary ammonium, coor, coor, on the containing terminate and receptor-targeted peptides for Radiolabeling peptide-containing receptor-targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0314-716 represent examples of F-18 labeled peptides used in the method of detecting a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                   Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 66; DB 20; 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY76817 standard; peptide; 8 AA.
                                                                                                                                                             Claim 14; Page 15; 22pp; English.
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           98WO-US18268
                                   97US-0057485.
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                                                             (IMMU-) IMMUNOMEDICS INC
                                                                                                           WPI; 1999-228967/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
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Misc-difference
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           03-SEP-1998;
                                   03-SEP-1997;
                                                                                     Griffiths GL;
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Best Local S
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conjugate that is capable of carrying at least 1 diagnostic or the cherapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targetal tissue and at least 1 arm (B) that specifically binds binds a targetale conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and tharapy. It is advantageous to raise bi-specific antibodies against a targetable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                  "D-form residue; modified with free amino acid
                                                                                                       group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bi-specific antibodies that bind specific target tissue and targeted
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100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leung S, McBride WJ,
/note= "D-form residue"
                                                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                               'note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY03714 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US13879.
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98US-0104156.
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                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-160561/14.
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Best Local Similarity
                                                                                                                                                                          Misc-difference 7
                                                                                                                                                                                                                                                Misc-difference 8
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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.

Fluorine-18 (F-18) labeled peptide 3.

(first entry)

08-JUN-1999

AAY03716;

'note= "D-form residue; optionally acetylated"

'note= "D-form residue; D-iodo-Tyr"

/note= "D-form residue"

Misc-difference 8

W09911590-A1 11-MAR-1999 98WO-US18268,

03-SEP-1998;

(IMMU-) IMMUNOMEDICS INC.

WPI; 1999-228967/19.

3riffiths GL;

'note= "D-form residue; D-iodo-Tyr"

'note= "D-form residue"

Misc-difference 5

Misc-difference

/note= "N-terminal acetylation"

Misc-difference Misc-difference

Modified-site

Synthetic

Location/Qualifiers

Radiolabeling thiol-containing peptides with fluorine-18

Claim 15; Page 15; 22pp; English.

m

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into peptide containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRRE2-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CH2)m-CRRE3-(CRRE3-(CH2)m-CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CRRE3-(CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                              D-form residue; optionally has a free or protected amino acid group"
                                                   /note= "optionally has a free or protected
   amino acid group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                  "D-form residue"
                                                                                                                                                                                     "D-form residue"
                                                                                                                                                                                                                                                                                                                           "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                              "D-form residue"
Location/Qualifiers
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                                                                                                                                                                                                                                           "D-form
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Key
Misc-difference 1
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into peptide containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)m-CRIR2 a fluorine-18 (F-18) comprises one of the two double bonded carbon atoms bears at least one leaving group comprising I, Br, Cl, azide, tosylate, nesylate, nesylate, nesylate, mesylate, mesylate, mesylate, mesylate, mesylate, mesylate, mesylate, nosylate, riflate, maleimide (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I, Br, Cl, azide, tosylate, mesylate, triflate, H, COMH2, COMH, COMH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl (optionally substituted by COMH2, COOH, OH, sulfonic acid, tertiary amine or quaternary ammonium, alkyl The method is used for Radiolabeling peptide-containing peptide-containing peptide-containing targeting carbon acid, tertiary amine or quaternary ammonium, cook, CONR2 or COR; and R = 1-6C alkyl or targeting carbon acid, tertiary amine or quaternary ammonium, alkyl and carbon acid, tertiary amine or quaternary ammonium, cook, CONR2 or COR; and R = 1-6C alkyl or targeting carbon acid, tertiary amine acid, tertiary amine carbon acid, acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               targeting vectors such as proteins, antibodies, antibody fragments and receptor- targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY03114-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for incorporating 18F radionuclide
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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85.7%;
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6; Conservative

Best_Local Similarity Matches 6; Conserv

Query Match

2 ywgcgyw 8

δ

AAY03716 ID AAY0: XX

; 0

Gaps

δλ g

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AAY42915 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                  Disulfide-bond Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1998;
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2 cywkcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 cywgcg
                                                                                 20-DEC-1999
                                                                                                                                                                                                                                                                                                                                       EP952159-A2
                                                                                                                                                                                                                                                                                                                                                                27-0CT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keri G, Sz
Horvath J,
                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                      AAY42915;
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  9
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               AAY42915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the use of certain heptapeptide somatostatin derivatives and/or phenylhydrazone derivatives for the preparation of medicaments possessing neurogenic and/or non neurogenic antiinflammatory and/or analgesic effects. The derivatives are used for treating pain and for treating neurogenic inflammation in the pathomechanism of rhinitis, bronchitis, bronchial asthma, arthritis, allergic conjunctivitis, urticaria, colitis and psoriasis. The present sequence is a preferred example of a heptapeptide somatostatin derivative for use in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helyes Z, Erchegyi J, Horvath A;
                                                                                                                                                                          Somatostatin derivative VZ-934 for antiinflammatory or analgesic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of somatostatin derivatives and phenylhydrazone derivatives for preparation of medicaments with neurogenic and/or non-neurogenic antiinflammatory and/or analgesic effects -
                                                                                                                                                                                     Somatostatin; antiinflammatory; analgesic; rhinitis; bronchitis; bronchial asthma; arthritis; allergic conjunctivitis; urticaria; colltis; psorlasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.6%; Score 42; DB 20; Length 7; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOS-) BIOSTATIN GYOGYSZERKUTATO-FEJLESZTO KFT
                                                                                                                                                                                                                                                                                                           /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szolcsanyi J, Pinter E,
                                                                                            AAY42908 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                              /note= "Thr-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 13; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99EP-0107392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98но-0000970
                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-582791/50.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
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2 ywgcgyw
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2 ywgkgyw
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                                                                                                                                                 20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                        EP952159-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   27-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cywgc
                                                                                                                                                                                                                                                          Synthetic
                                                                                                                      AAY42908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keri G,
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                                                        Somatostatin derivative VZ-1038 for antiinflammatory or analgesic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horvath A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of somatostatin derivatives and phenylhydrazone derivatives for preparation of medicaments with neurogenic and/or non-neurogenic antiinflammatory and/or analgesic effects -
                                                                                                    Somatostatin; antiinflammatory; analgesic; rhinitis; bronchitis; bronchial asthma; arthritis; allergic conjunctivitis; urticaria; colitis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOS-) BIOSTATIN GYOGYSZERKUTATO-FEJLESZTO KFT
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                           'note= "D-form residue"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szolcsanyi J, Pinter E,
I, Teplan I, Orfi L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB59639 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Gly-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 13; 20pp; English.
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98HU-0000970
(first entry)
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                                                                                                                                                                                                                                                                                                                                  Misc-difference 1
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                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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10-071247-2.closed.rag

Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;

Neuromedin B and somatostatin analogue #33.

(first entry)

23-MAR-2001

AAB59640;

AAB59640 standard; Peptide; 8 AA.

RESULT AAB59640

/label= OTHER /note= "N-(2-aminoethyl)-N-(2-thyminyl-1-oxo-ethyl) -glycine"

Location/Qualifiers

Key Modified-site

Synthetic.

eyelie.

note= "disulfide bond cyclises the peptide"

'note= "D-form residue"

Misc-difference Misc-difference

Disulfide-bond

/note= "D-form

Modified-site

Modified-site

/note= "C-terminal amide"

WO200075186-A1

14-DEC-2000

05-JUN-2000; 2000WO-US15396.

99US-0137655

04-JUN-1999;

BIOM-) BIOMEASURE INC

Morgan BA;

WPI; 2001-146787/15. Sadat-Aalaee D,

/label= OTHER

Bz1"

/label= OTHER /note= "modified

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(NMB). These can be used in the treatment of various cancers, anorexia, apporbyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal parcreatic pseudocysts and ascites, nesidoblastosis, external and hyperinaulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, dystrocosophageal reflux, duddenogastric reflux, cushing's syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, orthostatic hypotension, postprandial hypotension, panic attacks, diabetes mellitus, hyperlipidaemia, insulin insensitivity, syndrome X, peptic ulcers, arthritis, obesity, opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention provides analogues of somatostatin and neuromedin B
                                                                           NMB; somatostatin; analogue; Helicobacter pylori; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide compounds are somatostatin and neuromedin B receptor agonists, for treating a wide range of disorders e.g. cancer, gastrointestinal disorders and inflammatory disorders
                                                                                                                                                                                                                       'note= "disulfide bond cyclises the peptide"
                                                                                                                                                                                            'note= "modified by D-4-NO2"
                                           Neuromedin B and somatostatin analogue #32.
                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                /label= OTHER
/note= "modified by Bzl"
                                                                                                                                                                                                                                                       'note= "D-form residue"
                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overdose and gastrointestinal bleeding.
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 72; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                              /label= OTHER
                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2000; 2000WO-US15396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0137655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sadat-Aalaee D, Morgan BA;
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOM-) BIOMEASURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-146787/15.
                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                        WO200075186-A1
                                                                                                                                                Key
Modified-site
                                                                         Neuromedin B;
                                                                                                                                                                                                                                                                                                  Modified-site
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               23-MAR-2001
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                                                                                                                    Synthetic.
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                                                                                         cyclic.
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(NMB). These can be used in the treatment of various cancers, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic sclerosis, external and internal pancreatic pseudocysts and ascites, nesidoblastosis, external and hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastrocesophageal reflux, dudenogastric reflux, Cushing's syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, orthostatic hypotension, postprandial hypotension, panic attacks, diabetes mellitus, hyporlipidaemia, insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides analogues of somatostatin and neuromedin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insensitivity, syndrome X, peptic ulcers, arthriffs, obesity, opioid overdose and gastrointestinal bleeding.
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Pred. No. 6.4e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.1%;
Best Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA;
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Gaps

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Length 8;

Score 39; DB 22; Length 8; Pred. No. 6.4e+05; 0; Mismatches 2; Indels

59.1%; 71.4%;

Conservative

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Query Match Best Local Similarity Matches 5; Conserv

New polypeptide compounds are somatostatin and neuromedin B receptor agonists, for treating a wide range of disorders e.g. cancer, gastrointestinal disorders and inflammatory disorders

Claim 15; Page 73; 85pp; English.

Length 8;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue are transfer and instance brispecific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable
                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ζ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "D-form iodo-Tyr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Page 61; 76pp; English.
                                                                                                                                                                                                           AAY76818 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-160561/14
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Modified-site
      cywgcgy
                                                          2 cywkcty
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                                                                                                                                                                                                                                                                                                                             28-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                      AAY76818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                            Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;
                                                                                                                                                                                                                                                                                                                                                                  /note= "optionally N-(3-indolylacetyl)-L-phenylalanine,
                                                                                                                                                                                                                                                                                                                                                                         N-(2-aminoethyl) -N-(2-thyminyl-1-oxo-ethyl) glycine, N-(2-aminoethyl) -N-(2-cytosinyl-1-oxo-ethyl) glycine, 5-(4-methyl-2-nitrophenyl) -2-furoic acid, isonipecotic acid or nicotinuric acid.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide compounds are somatostatin and neuromedin B raagonists, for treating a wide range of disorders e.g. cancer, gastrointestinal disorders and inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "disulfide bond cyclises the peptide"
                                   Indels
DB 21; Leu. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "optionally D-form residue"
                                                                                                                                                                                                                                   Neuromedin B and somatostatin analogue #34.
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= OTHER
/note= "C-terminal amide"
        Score 37; 1
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= OTHER
/note= "modified by Bzl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D-form residue"
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 73; 85pp; English.
                                                                                                                                                        AAB59641 standard; Peptide; 8 AA.
                                   ;
                                                                                                                                                                                                                                                                                                                                                      /label= OTHER
          56.1%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2000; 2000WO-US15396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0137655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sadat-Aalaee D, Morgan BA;
                                                                                                                                                                                                          (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-146787/15.
                        Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200075186-A1
                                                             2 умдсдум 8
                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                       2 ywhkgyw
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                                                                                                                                                                                                          23-MAR-2001
                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                  AAB59641;
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; 0

Gaps

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while still bonded to the solid phase. The products of the invention have cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits and the tyrosine kinase activity of various human stomach cancer cell lines and thus inhibits cellular proliferation. The heptapeptide (I) described in the invention is a somatostatin analog which shows strong antitumor eativity in vitro and in vivo. The SP synthesis method gives (I) is more which the cyclization is carried out after cleaving the peptide from the which the cyclization is carried out after cleaving the peptide from the sin. The solution method is also a simple synthesis of (I) in high yield; typically the tert-buty1-protected precursor can be oxidized in a yield of 70-80%. Ax51896-x51900 repersent peptides used in the synthesis of biostatin T7232 described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; cancer; neoplasm; malignancy; psoriasis; regulation of; release of; growth hormone; insulin; glucagon; prolactin; inhibit exopeptidase; inhibit tumour growth; tumour transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G, Csuka O, Horvath A, Horvath J, Idei
Seprodi J, Szoke B, Teplan I, Vadasz Z;
bedi J, Szoeke B, Mezo I, Templan I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New octa:peptide or hepta:peptide somastatin analogues - as tyrosine kinase inhibitors for treating tumours and psoriasis, and for regulating hormone release
                                                                                                                                                                                                                                       Length 6;
                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somatostatin analogue tyrosine kinase inhibitor #3.
                                                                                                                                                                                                                                     Score 34; DB 21;
Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSIGNAL KUTATO FEJLESZTO KFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; cancer; neoplasm; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             AAR27179 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "D-form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form"
                                                                                                                                                                                                                                    51.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mezoe I, Sepr
i G, Seproedi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bokonyi G,
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                            6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keri G, Mezor
Boekoenyi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KERI/) KERI
(BIOS-) BIOSI
                                                                                                                                                                                                                                                                                            cywgc 5
                                                                                                                                                                                                                                                                                                                       cywkc 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP505680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balogh A,
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR27179;
                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                               AAR27179
          0;
hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastrooesophageal reflux, duodenogastric reflux, Cushingy s syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, paget's disease, polycystic ovary disease, orthostatic hypotension, panic attacks, diabetes mellitus, hyperinjdaemia, insulin insensitivity, syndrome X, peptic ulcers, arthritis, obesity, opioid overdose and gastrointestinal bleeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for the solid phase (SP) synthesis of biostatin (TT 232) (I) which includes closing the disulfide bridge by oxidation of the completely or partially constructed peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor; cellular proliferation inhibition; somatostatin; antitumor.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biostatin preparation in high yield by solid synthesis, including closure of disulfide bridge before cleavage from support, useful
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Thr(tBu) with C-terminal amide group"
                                                                                                                                                                         Score 35; DB 22; Length 8;
Pred. No. 6.4e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Biostatin TT232 synthesising peptide 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Ddz-Cys(Acm)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Tyr-(tBu)"
                                                                                                                                                                                                                                                                                                                              AAY51899 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Cys(Acm)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 25; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Lys(Z)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birr C;
                                                                                                                                                                         53.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP06131.
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Braum G, Lifferth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-224663/19.
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antitumor agent -
                                                                                                                              8 AA;
                                                                                                                                                                                                                                                      2 cfwkcty 8
                                                                                                                                                                                                                              1 cywgcgy 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200011032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000
                                                                                                                                                                       Query Match
Best Local Si
Matches 4;
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                            AAY51899;
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Idei M;

7 AA;

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AAW18456;
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          Sequence
                                                                                                                                          14
                                                               Matches
                                                                                                                                                    AAW18456
                                                                                                                                          RESULT
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SO
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                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somatostatin agonists include the somatostatin analogs shown in AARS6777 848 and AAR6074 83. These peptides are used in the invention to inhibit the accelerated growth of tumours. The growth is induced surgically and the tumour is of epithelial origin, eg. lung or colon tumours or partic. prostate or breast tumours, or melanoma. The peptides are known inhibitors of cancer cell growth and are partic. applied to the site of trauma, topically or subcutaneously.
                                                                                                                                                               Gaps
          and selective pharmacological action than somatostatin. It has a structure inhibiting the activity of exopeptidases. It can be used in medicaments to inhibit tumour growth or the activity of tyrosine kinase enzymes involved in tumour transformation. It is also useful
                                                    for regulating the release of growth hormone, insulin, glucagon and prolactin. It may also be used to inhibit pathological processes such as psoriasis, elicited by the pathological proliferation of
                                                                                                                                                                                                                                                                                                                            Somatostatin analog 41 - acts as agonist to inhibit tumour growth.
This peptide is a somatostatin analogue showing more advantageous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting accelerating tumour growth after trauma, esp surgery by treatment with somatostatin or its agonists, esp applied to the site of trauma
                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                               somatostatin; agonist; analog; accelerating tumour growth; t
surgery; treatment; solid primary tumour; metastatic tumour;
inhibition; tissue trauma; ulcer.
                                                                                                                                        Score 34; DB 13; Length 7; Pred. No. 6.4e+05;
                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "H-Phe; D-form residue"
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12; 33pp; English.
                                                                                                                                                                                                                                                              AAR56817 standard; peptide; 7 AA.
                                                                                                                                        51.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US01412
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moreau J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-279685/34.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 4
                                                                                                         7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                    1 cywgc 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38-FEB-1994;
                                                                                                                                                                                                       cywkc 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1993;
                                                                                                                                                                                                                                                                                                      20-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9418231-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bodgen AE,
                                                                                     skin cells
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                 AAR56817;
                                                                                                           Sequence
                                                                                                                                                                                                                                         13
                                                                                                                                                              Matches
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide(s) - which inhibit the release of for the treatment and diagnosis of tumours
                                                      ;
0
     Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth hormone; tumour; Antarelix; Lanreotide; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "L-2-methyltryptophan amide"
Score 34; DB 15;
Pred. No. 6.4e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somatostatin analogue heptapeptide.
                                                                                                                                                                                                                                                                                                        AAW18456 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 15; 21pp; English.
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/note= "L-2-me
     51.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New somatostatin analogue growth hormone, used e.g.
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                               2 cywkc 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9705167-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1997
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                                                                                                                  1 cywgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acromegaly
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                                                                                                                                                                                                                                                                      Somatostatin; agonist; inhibitor; fibrosis; kidney; lung; liver; skin; chemchkrapy; glomerulonephritis; diabetes; cirrhosis; nasal polyposis; allograft rejection; infection; human immune deficiency virus; therapy; central nervous system; intraocular fibrosis.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting fibrosis by administration of somatostatin or its agonists – particularly in lung, liver, kidney and skin, or where caused by chemotherapy
                                         ;
0
Score 34; DB 18; Length /;
Pred. No. 6.4e+05;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 24pp; English.
                                                                                                                                                         AAY22068 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                               note= "H-D-Phe"
           51.5%;
80.0%;
                                                                                                                                                                                                                                            Somatostatin agonist peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0705790
                                                                                                                                                                                                                  (first entry)
         Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Culler MD, Kasprzyk PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BIOM-) BIOMEASURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-207029/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                 1 cywgc 5
                                                                                 ||| |
2 cywkc 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1996;
                                                                                                                                                                                                                  27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9808528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1998
                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                       AAY22068;
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Gaps

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Score 34; DB 19; Length 7; Pred. No. 6.4e+05; 0; Mismatches 1; Indels

51.5%; 80.0%;

4; Conservative

1 cywgc 5

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Query Match Best Local Similarity Matches 4; Conserv

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Cywkc (
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Search completed: August 12, 2002, 17:14:32 Job time: 245 sec

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10-071247-2.closed.rai

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Sequence 8, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
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Sequence 128, App
Sequence 919, App
Sequence 919, App
                                                                 August 12, 2002, 17:14:59; Search time 20.43 Seconds (without alignments) 9.565 Million cell updates/sec
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Sequence 2, Ap
Sequence 13, A
Sequence 14, A
Sequence 1, Ap
Sequence 1, Ap
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Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-488-659A-128
US-09-3082-3048-919
US-09-3082-980B-8
US-08-286-980B-8
US-08-948-7
US-09-484-318-1
US-09-484-318-1
US-09-484-319-8
US-09-484-311-1
US-09-484-321-1
US-09-325-769-2
US-09-325-769-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-530-566-10
                                                                                                                                                                                                        231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                              1 cywgcgyw 8
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66
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                                                                                                                                                                      BLOSUM62
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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                                                                                                                                              Sequence:
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Sequence 5, Appli
Sequence 8, Appli
Patent No. 51889
Sequence 12, Appl
Sequence 110, App
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                            Sequence 21, Appl
Patent No. 5190920
Patent No. 5606208
Sequence 7, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 29, Appli
    Sequence 10, Ag
Sequence 10, Ag
Sequence 139, Ag
Sequence 139, Ag
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 128, Application US/08487006
; Patent No. 5641861
; GENERAL: INFORMATION;
; APPLICANT: Booley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
; TITLE OF INVENTION: Agonists and Antagonists
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 335-9001
TELEPHONE: (619) 535-9049
INFORMATION FOR SEG ID NO: 128:
SEQUENCE CHARACTERISTICS:
US-09-195-726-10
US-09-067-755-10
US-08-488-659A-139
US-09-329-350-8
US-09-329-350-8
US-09-329-350-8
US-09-329-350-8
US-08-520-535-12
US-08-811-492-110
US-08-483-434A-11
US-08-498-120-6
US-08-483-434A-11
US-08-498-120-6
US-08-498-120-6
US-08-498-120-6
US-08-498-120-6
US-08-498-120-11
US-08-498-120-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide LOCATION: 1..7
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TOPOLOGY: linear
 92122
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US-08-487-006-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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/note= "With the exception of Gly in position 6, all amino acids are D-amino acids."

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/note= "Amino acid is amidated the C-terminal."

OTHER INFORMATION: COTHER INFORMATION: US-08-487-006-128

NAME/KEY: Peptide

LOCATION:

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Query Match
Best Local Similarity
Matches 4; Conserva
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APPLICANT: Barney, 3
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US-09-315-304B-919
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US-08-282-980B-8
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                                    0; Indels
 Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid is amidated at
the C-terminal."
                                                                                                    RESULT 2
US-08-488-659A-128
Sequence 128, Application US/08488659A
Fatent No. 5919877
GENERAL INFORMATION:
APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCE 223
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,659A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
 Score 28; DB 1; Pred. No. 1.7e+05;
                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATOCKNET/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1705
TELECHONIC. (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino_acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-082-279B-919
; Sequence 919, Application US/09082279B
 42.48;
75.08;
Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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OTHER INFORMATION:
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) OTHER INFORMATION:
US-08-488-659A-128
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SEQ ID NO 919
LENTH: B
LENTH: B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.4%; Score 28; DB 4; Length 8; Best Local Similarity 80.0%; Pred. No. 1.7e+05; Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.4%; Score 28; DB 4; Length 8; 80.0%; Pred. No. 1.7e+05; ive 0; Mismatches 1; Indels
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SENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis BPLICANT: Lambert, Dennis BPLICANTON: PHARMACOKINETIC PROPERTIES
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 919, Application US/09315304B Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Core polypeptide US-09-082-2798-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Core polypeptide US-09-315-304B-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/08282980B
; Patent No. 5932189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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/label= Cyclic /note= "The amino terminus and carboxyl terminus are linked by a covalent bond; the amino terminus is substituted with a methyl group."
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Patent No. 5759542

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: ARDIOVASCULAR AND OTHER DISEASES
OORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: 1..3
COTHER INFORMATION: /label= Variant residues
COTHER INFORMATION: /note= "The Trp is in the D conformation."
US-08-931-095-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Query Match

40.9%; Score 27; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                          CALF: PUBOUD COMPUTER EAGLABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,095
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6017512nan, Kevin E
REGISTRATION NUMBER: 35,303
REBERRICE/POCKET UNBER: 92,385-00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 Or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
LCGATION: 1..6
OTHER INFORMATION: /Iabel.
OTHER INFORMATION: /note=
OTHER INFORMATION: are lin
OTHER INFORMATION: is sub.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                       COUNTRY: U
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NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
OTHER INFORMATION: are linked by a covalent bond."
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) OTHER INFORMATION: /label= Variant residues
) OTHER INFORMATION: /note= "The Trp is in the D conformation"
US-08-282-980B-8
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; Patent No. 6017512
; GENERAL INFORMATION:
    APPLICANT: Dean, Richard T.
    APPLICANT: Lister-James, John
    TITLE OF INVENTION: Radiolabeled Peptides
    NUMBER OF SEQUENCES: 26
    CORRESPONDENCE ADDRESS:
    ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
    STREFT: 300 South Wacker Drive, 32nd Floor
                  APPLICANT: Dean, Richard T.
APPLICANT: Dean, Richard T.
APPLICANT: McBride, William
APPLICANT: Lister-James, John
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMCDONNell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,980B
FILING DATE: 29-UUL-1994
CLASSIFCATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No. 5932189nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
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Best Local Similarity 100.(
Matches 3; Conservative
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-913-0002
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GENERAL INFORMATION:
                                                                                                                                                                                                                               Chicago
                                                                                                                                                                                                                                                                                    USA
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CITY: Chicago
                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 60606
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US-08-931-095-5
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Octreotide
NAME/KEY: SITE
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100.0%; Pred. No. 1.7e+05;
live 0; Mismatches 0; Indels
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APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Brajagopalan, Raghavan
APPLICANT: Brajagopalan, Raghavan
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,319
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO ELENGTH: 8
LENGTH: 8
                                                                                                                Sequence 8, Application US/09484318
; Sequence 8, Application US/09484318
; Patent No. 6180085
; GENERAL INFORMATION:
; APPLICANT: Achilefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Bagajo, Joseph E.
; TILLE OF INVENTION: NOVEL DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,318
; CURRENT FILING DATE: 2000-01-18
; SEQ ID NO 8
; SEQ ID NO 8
; LENGTH: 8
; LENGTH: 8
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OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
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OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : LOCATION: (4); OTHER INFORMATION: This is D-tryptophan US-09-484-318-8
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Best Local Similarity
Matches 3; Conserva
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NAME/KEY: SITE
1 cyw 3
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2 CYW 4
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US-09-484-318-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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LOCATION: (8)
OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-318-1
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40.9%; Score 27; DB 4; Lost Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa is D- -Naphthylalanine US-08-286-748B-7
                 APPLIANT NORDER: 05/05/200/7450
CLASSIFICATION: 424
PRIOR APPLICATION 1044
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: J. Peter Fasse
RECISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/01301
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
ITILE OF INVENTION: NOVEL DYES
FILE REFERRNCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,318
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 8
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OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULEID
LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
    APPLICATION NUMBER: US/08/286,748B
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 3; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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2 CYW 4
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Sequence 8, Application US/09484320;
Sequence 8, Application US/09484320;
Sequence 8, Application US/09484320;
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastrng
CURRENT APPLICATION UNDBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 8
LENGTH: 8
                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Octreotide
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
LOCATION: (2)
LOCATION: (2)
LOCATION: (2)
NAME/KEY: SITE
NAME/KEY: SITE
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OTHER INFORMATION: This is D-phenylalanine
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                    40.9%; Score 27; DB 4; Length 8; ilarity 100.0%; Pred. No. 1.7e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                         LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
NAME/KEY: SITE
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US-09-484-321-1
; Sequence 1, Application US/09484321
                                LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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NAME/KEY: SITE
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               SEQ ID NO 1
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APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Bajagopalan, Raghavan
APPLICANT: Bugaj, Joseph E.

TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastrng
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
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                                                               COTHER INFORMATION: This C-terminal residue ends with a hydroxyl US-09-484-319-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rajagopalan, Raghavan APPLICANT: Rajagopalan, Raghavan APPLICANT: Bugai, Joseph E. TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES FILE REFERENCE: DNA STRING CURRENT APPLICATION NUMBER: US/09/484,319 CURRENT FILING DATE: 2000-01-18 NUMBER: PS EQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: This is D-phenylalanine MAME/KEY: DISULEID LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (4) -
; OTHER INFORMATION: This is D-tryptophan
US-09-484-319-8
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09484319
Patent No. 6180086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09484320 Patent No. 6180087
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achilefu, Samuel
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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APPLICANT: ACHILEÍ
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2 CYW 4
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LENGTH: 8
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; Sequence 8, Application US/09484321
; Patent No. 6183726
; GENERAL INFORMATION:
    APPLICANT: Achiledu. Samuel
    APPLICANT: Achiledu. Samuel
    APPLICANT: Bajagobalan, Raghavan
    APPLICANT: Bajagobalan, Raghavan
    APPLICANT: Bajagobalan, Raghavan
    APPLICANT: Bajagal, Oseph E.
    TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
    FILE REFERENCE: DNA STRING
    CURRENT FILING DATE: 2000-01-18
    NUMBER OF SEQ ID NOS: 8
    SOFTWARE: Patentin Ver. 2.1
    SEQ ID NO 8
    LENGTH: 8
    TYPE: PRT
    ORGANISM: Artificial Sequence
    FEATURE:
    ORGANISM: SITE
    LOCATION: (1)
    COTHER INFORMATION: Description of Artificial Sequence: CATION: (1)
    COTHER INFORMATION: This is D-phenylalanine
    NAME/WEY: DISULPID
    LOCATION: (2) '''
    LOCATION: (2) '''
    LOCATION: (2) '''

                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Octreotide

NAME/REY: SITE

LOCATION: (1)

OTHER INFORMATION: This is D-phenylalanine

NAME/REY: DISULFID

LOCATION: (2)...(7)

NAME/REY: SITE

LOCATION: (4)

OTHER INFORMATION: This is D-tryptophan

NAME/REY: SITE

LOCATION: (8)

COTHER INFORMATION: This is D-tryptophan

NAME/REY: SITE

LOCATION: (8)

COTHER INFORMATION: This C-terminal residue ends with a hydroxyl

US-09-484-321-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                 GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajaqopalan, Raghavan
APPLICANT: Bajaqopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
FILE REPRENCE: DNA STRING;
CURRENT APPLICATION NUMBER: US/09/484,321
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 8
LENGTH: 8
LENGTH: 8
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: This is D-tryptophan US-09-484-321-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
Patent No. 6183726
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cyw 3
| I j
| Db 2 CYW 4
| Search completed: August 12, 2002, 17:15:00
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(without alignments)
17.168 Million cell updates/sec
                                                                                                            August 12, 2002, 17:18:23 ; Search time 51.76 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                            747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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| SIDS1/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1981.DAT:*
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| SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseqp-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1991.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Fluorine-18 (F-18) Fluorine-18 (F-18) Immunoqenic peptid	Immunogenic peptid H2 homologue of pr	KRE5. Saccharomyc Yeast KRE5. Sacch Fluorine-18 (F-18)	Immunogenic perid Human novel secret Human protein SEQ
SUMMARIES	ID	AAY03714 AAY03716 AAY76816	AAY76818 AAB18511 AAB36780	AAB72446 AAY03715	AAY76817 AAU16277 AAB99111
	DB	20 20 21	21	22	21 22 22
	å Query Match Length DB	885	841 1365	1365	164 152
đ	Query Match	100.0 100.0 100.0	86.4 81.4 79.7	79.7	76.3
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Human protein SEO		æ	Drosophila melanog	Streptococcus pneu		H	Schizos	ب د .	1 5' EST	>	VH4715-11nker-VH34	HindIII-EcoR1 inse	linker-	I-ECOR1	nic M3	_	Q		ic Iq sup	Ï	Si	Ø	s thali	Sequence encoded b		õ	Ω.	U	U	Ö	U	Ę	human
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ALIGNMENTS

RESULT

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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
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                                                                                                                                                                                                                                                            Fluorine-18 (F-18) labeled peptide 1.
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                                    AAY03714 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                     The invention relates to a method for incorporating 18F radionuclide
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                                                                                                                                                                                                            Radiolabeling thiol-containing peptides with fluorine-18
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100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal acetylation"
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                                                                                                                                                                                                                                                    Claim 13; Page 15; 22pp; English.
                  98WO-US18268.
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                             (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                         WPI; 1999-228967/19.
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The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CR1R2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded arbon bears at least one leaving group comprising 1, Br. Cl. azide, tosylate, mesylate, nesylate, no mean = 0-2; n+m = 0-2; x = 1, Br. Cl. azide, tosylate, mesylate, nosylate, rifilate, M. R2 = 1, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, H. CONH2, COCH, OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl or phenyl. The method is used for Radiolabeling peptide-containing peptide containing tertiary amine or quaternary ammonium, alkyl or phenyl. The method is used for Radiolabeling peptide-containing receptor-targed peptides for was in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAV0314-716 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
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/note= "D-form residue; optionally acetylated"
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                                                                   "D-form residue; D-iodo-Tyr'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59; DB 20;
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                   /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 15; 22pp; English.
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                                                                       'note=
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Best Local Similarity
Matches 8; Conserv
                                       Misc-difference 7
                                                                                                       Misc-difference 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000
                                                                                                                                                                                                           WO9911590-A1
                                                                                                                                                                                                                                                                                                                                               03-SEP-1998;
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Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.

'note= "acetylated D-form residue"

'note= "D-form iodo-Tyr"

Misc-difference 8

W09966951-A2

39-DEC-1999

22-JUN-1999; 22-JUN-1998; 14-OCT-1998;

/note= "D-form residue"

'note= "D-form iodo-Tyr"

Misc-difference 3 Misc-difference 5 Misc-difference 7

Misc-difference

Modified-site

Synthetic

Location/Qualifiers /note= "acetylated" 'note= "D-form residue"

Immunogenic peptide for bi-specific antibody recognition.

(first entry)

28-APR-2000

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conjugate that is capable of carrying at least I diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable
                                                                                                                    "D-form residue; modified with free amino acid
group, protected amino acid group, chelating
agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                           Bi-specific antibodies that bind specific target tissue and targeted
                              __note= "free amino acid group, protected amino acid
group, chelating agent or a metal-chelate
complex"
                                                                                                                                                                                                                                                                                                                                    Leung S, McBride WJ,
                                                                           "D-form residue"
                                                                                                                                                                /note= "D-form residue"
                                                                                               "D-form residue"
                                                                                                                                                                                      /note= "D-form residue"
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                           98US-0090142.
98US-0104156.
                                                                                                                                                                                                                                                        99WO-US13879
                                                                                                                                                                                                                                                                                                                                 Griffiths GL,
                                                                                                                                                                                                                                                                                                             (IMMU-) IMMUNOMEDICS INC.
                                                                                                 "note=
                                                                                                                      /note=
                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-160561/14.
                                                              Misc-difference 3
                                                                                                                                                    Misc-difference 8
                                                                                                          Misc-difference 6
                  Misc-difference
                                                                                    Misc-difference
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                            WO9966951-A2
                                                                                                                                                                                                                                                       22-JUN-1999;
                                                                                                                                                                                                                                                                           22-JUN-1998;
                                                                                                                                                                                                                                                                                       14-OCT-1998;
                                                                                                                                                                                                                                  29-DEC-1999
                                                                                                                                                                                                                                                                                                                                 Hansen HJ,
                                                                                                                                                                                                                                                                                                                                                                                         conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprishing administering a bi-specifically antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.4%; Score 51; DB 21; Length 8; 87.5%; Pred. No. 6.4e+05; 1ve 0; Mismatches 1; Indels
Claim 23; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 87.5
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gywgkgyw 8
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1 gywhkgyw 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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; 0

Gaps

ó;

Length 9; Indels

100.0%; Score 59; DB 21; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0;

8; Conservative

1 gywgkgyw 8

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Best Local Similarity

Matches

Query Match

RESULT AAB18511

AAY76818 standard; peptide; 8 AA.

AAY76818

RESULT
AAY76818
ID AAY76
XX
AC
AC
XX

Bi-specific antibodies that bind specific target tissue and targeted

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McBride WJ,

Leung S,

Hansen HJ, Griffiths GL, (IMMU-) IMMUNOMEDICS INC.

WPI; 2000-160561/14.

conjudates

98US-0090142. 99WO-US13879

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27-JUL-2000; 2000WO-CA00883
            Saccharomyces cerevisiae.
                                                                                                                                                                                                                   N-PSDB; AAQ38899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200112845-A1
                                                                                            05-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2001.
                                      US5194600-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2001
                                                                   16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast KRE5
                                                                                                                                                                             Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB72446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB72446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a H2 homologue of a prolyl tripoptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripoptidase has an amidolytic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodontal disease such as ginglivitis and periodontilis caused by
                                                                                                                                                                                                                                                                                                                                                                                                          Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis
                                                                                                           Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast; cell wall; beta-glucan; assembly; pathway; KRE1; KRE5; growth; secretory; O-linked mannose; (1>6)-beta-glucan; epistasis; morphology; hydrophilic; glycoprotein; COOH-terminal; endoplasmic reticulum; ER; retention signal; antifungal agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 21; Length 841;
Pred. No. 54;
0; Mismatches 1; Indels
                                                                                12 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR36780 standard; Protein; 1365 AA.
AAB18511 standard; protein; 841 AA.
                                                                                                                                                                                                                                                                                        UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                          Banbula A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Fig 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.4%;
                                                                                                                                                                                                                                                           99US-0123148.
                                                                                                                                                                                                                                  03-MAR-2000; 2000WO-US05551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                    (first entry)
                                                                                                                        gingivitis; periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis.
                                                                                                                                                   Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                          Fravis J, Potempa J,
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-594181/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     (TRAV/) TRAVIS J.
(POTE/) POTEMPA J.
(BANB/) BANBULA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   719 ywgsgyw 725
                                                                                                                                                                             WO200052147-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ywgkgyw 8
                                                                                                                                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1993
                                                    L5-JAN-2001
                                                                                                                                                                                                        08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                           AAB18511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT AAR36780
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The sequences given in AAR34785 and AAR36780 represent proteins which participate in a yeast cell wall beta-glucan assembly pathway.

These proteins represent KREI and KREF respectively, and are essential for normal cell growth. KREI is a Ser/Thr rich protein protein probably probably probably through addition of O-linked mannose healthaly modified, probably through addition of O-linked mannose cesidues. Gene disruption of the KREI locus leads to a 40% reduced cesidues. Gene disruption of the KREI locus leads to a 40% reduced defects in cell wall (1>6) beta-glucan. Mutations at KRE5 also caused defects in cell wall (1>6) beta-glucan production and appears to be defects in cell wall (1>6) beta-glucan production and appears to be objected in which contains the COOH-terminal endoplasmic reticulum (ER) retention signal (His-Asp-Glu-Leu). Deletion of the KRE5 gene results in cells with aberant morphology and extremly compromised growth. KREI and KRE5 are useful as tools for the in vitro screening of antifugal agents which inhibit fungi pathogenic to plants and animals. The genes can be used to produce mutants for in vivo screening of antifungal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; KRE5.
                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding genes which participate in beta-glucan assembly - useful for producing mutants for in-vivo screening of antifungal agents and providing tools for in-vitro screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                    Sommer SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                               (ROYA-) ROYAL INST ADVANCEMENT LEARNING.
                                                                                                                                                                                                                    Meaden P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Columns 38-44; 24pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB72446 standard; Protein; 1365 AA.
                                                                                                                                                                                                                Hill K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.7%;
75.0%;
90US-0488316
                                                                           90US-0488316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
                                                                                                                                                                                                                    Bussey H,
                                                                                                                                                                                                                                                                                            WPI; 1993-109384/13.
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98WO-US18268.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   умдсдум 8
                                                                                                        Griffiths GL;
                                     03-SEP-1998;
                                                            03-SEP-1997;
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              11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY76817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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ID AAY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                            The present invention relates to a method for determining the effect of a activity. The method comprises exposing an acceptor substrate for UGGT a labelled donor in the presence of the test sample and UGGT. The method is useful in a plucosyltransferase exsay and kinetics meathod is useful for determining UGGT activity. In particular, the method is useful in plucosyltransferase assay and kinetics measurement for determining UGGT activity. In particular, the method is determining UGGT activity, UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto a paparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence was used in a sequence homology comparison with rat UGGT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                 Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "N-terminal acetylation; optionally has a free
or protected thiol group"
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "D-form residue; optionally has a free protected thiol group"
                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 22; Length 1365;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
                                                        Bergeron JJM, Thomas DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (F-18) labeled peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                         Disclosure; Fig 9; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY03715 standard; peptide; 8 AA.
                                (CANA ) NAT RES COUNCIL CANADA
          99us-0376330.
                                                                                                                                                                                                                                                                                                                                                                   79.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.v
6; Conservative
                                                      Tessier DC, Dignard D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                    the presence of UGGT
                                                                           WPI; 2001-218358/22.
                                                                                                                                                                                                                                                                                                                                 1365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1234 gywkegyw 1241
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                                                                                                                                                                                                                                                                                                                                                                                                              1 gywgkgyw 8
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          18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AAY03715
qq
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into peptide-containing targeting vectors for use in clinical positron mission terrors. Care in clinical positron mission terrors for the peptides with the peptide-containing thiol-containing peptides with comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2-(CH2)m-CRIR2
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protected amino acid group, chelating agent or a
metal-chelate complex"
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide for bi-specific antibody recognition.
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                                                                                                                                                                                                                                              Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%; Score 45; DB 20;
85.7%; Pred. No. 6.4e+05;
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0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                        Claim 14; Page 15; 22pp; English.
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(IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                WPI; 1999-228967/19.
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Best Local Similarity
Matches 6; Conserv
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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
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cytostatic; cardiant, vasotropic; cerebroprotective; nootropic;
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                  /note= "D-form residue; modified with free amino acid
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                                                             group, protected amino acid group, chelating agent or a metal-chelate complex"
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/note= "D-form residue"
Misc-difference 3
                                                                                                                  /note= "D-form residue"
                             'note= "D-form residue"
                                                                                            'note= "D-form residue"
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                                                                                                                                                                                 99WO-US13879
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98US-0104156
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Best Local Similarity
``hes 6; Conserv?
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                                                                                 Misc-difference 7
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                                                                                                       Misc-difference
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vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0230437.
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2000US-0225266.
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20000S-0226279.
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2000US-0231243.
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24-FEB-2000;
02-MAR-2000;
17-MAR-2000;
17-MAR-2000;
18-MAY-2000;
07-JUN-2000;
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18-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
                                                                                                                            Homo sapiens.
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05-SEP-2000;
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08-SEP-2000;
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14-AUG-2000;
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30-AUG-2000;
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26-JUL-2000;
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2000US-0236368.
2000US-0236370.
2000US-02370370.
2000US-0237037037.
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2000US-0234997.
2000US-0234998.
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2000US-0244617.
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2000US-0251868.
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14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 22-SEP-2000; 22-SE
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05-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prewnt, treat or annellocate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They mans, mice, are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoasays e.g. radioimmunoasays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other and sonders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other disorders e.g. conneal infection, and many other disorders e.g. cuburn, to maintain organs before transplantation, for supporting call culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present capacitic and other nutritional components. The present
                                                                                                                                                                                                                                                         New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, antiarthritic, cardiant, monoclonal antibody; keloid, arthritis, Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.3%; Score 45; DB 22; Length 164; ilarity 75.0%; Pred. No. 30; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 1230; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB99111 standard; Protein; 152 AA.
                                                                                                                                                              Ruben SM;
                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0254099.
                                                                             05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID 4.
                                                                                                                                                          Rosen CA, Barash SC,
                                                                                                                                                                                                 WPI; 2001-488783/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                      N-PSDB; AAS26264.
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Ma Y;

Cao Y,

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to ercoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to production of other lead to the cell in the cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y
Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.6%; Score 44; DB 22; Length 10
75.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #19161.
                                                                                                                                                              useful in diagnosis and gene therapy
                                                                                                                                                                                                 Claim 20; Page 420; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG19170 standard; Protein; 1180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
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                                                                              WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1090 AA;
    Liu C, I
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001 gywgdgew 1008
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                                           Yang Y,
                                                                                                    N-PSDB; AAK53220.
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    Tang YT,
Zhao QA,
                                         Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                          Human monoclonal antibodies recognizing human TGF-beta II receptor, useful for treating TGF-beta associated diseases such as tissue fibrosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 22; Length 152;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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Mismatches
                                                                                                                                                                                                                                                                                                                    Claim 10; Page 94-95; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM80087 standard; Protein; 1090 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.68;
75.08;
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2000US-0560875.
2000US-0598075.
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10-SEP-2000; 2000US-0654936-

15-SEP-2000; 2000US-0653561.

20-OCT-2000; 2000US-0693325-

30-NOV-2000; 2000US-0728422.
                                           18-NOV-1999; 99JP-0328681.
08-NOV-2000; 2000JP-0340216.
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      17-NOV-2000; 2000WO-JP08129
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                                                                                                      (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                            Kamada M;
                                                                                                                                                                                 WPI; 2001-343825/36.
N-PSDB; AAH41153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 gywgfdyw 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gywgkgyw 8
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01-SEP-2000;
15-SEP-2000;
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20-JUN-2000;
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                                                                                                                                            Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                 fibrosis
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Matches

AAM80087

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Gaps

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sequences of anti-adipocyte monotonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a chy complement mediated lysis. The antibodies may be labeled with a cused in methods of diagnosis in human subjects e.g. to determine the presence of adipocytes on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
                        AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 35820; 21pp. + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                              71.2%; Score 42; DB 22; Length 121; 71.4%; Pred. No. 59; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 35820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB69676 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
''hac 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                        121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 ywgrgqw 116
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                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The carbon class are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypetide and polynucleotide sequences have applications in capposable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010 ABG30377 represent novel human and and activity of amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 22; Length 1180;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-adipocyte monoclonal antibody heavy chain, FAT 91.
                                Claim 20; SEQ ID No 49529; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02601 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.6%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence . 1180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 gywgdgew 1098
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N-PSDB; AAS03501.
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Claim 1; Page 156; 182pp; English.